FIG.1A

```
                148       178       208       238       268       298
        FRI-1   ALLVFLDIIEWTTQETFPPKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPD
                                                |: | ||:||   |  ||    |:| :| |
SW:TNR2_HUMAN   HALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
                        30        40        50        60        70        80

                328
        FRI-1   YSYTDSWHTS
                 :||: |:
SW:TNR2_HUMAN   STYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL
                        90       100       110       120       130       140
```

FIG.1B

```
                .         .         .         .         .
        FRI-1    69 YLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCV.PCPDY.SYTDSW
                    |  |.  ...   | .| || :|  .|    : | |  || :   |.| .
  TNFR profile    6 YHYYDQNGRMCEECHMCQPGHFLVKHCKQPKRDTVCHKPCEPGVTYTDDW

        FRI-1   116 H
                    |
  TNFR profile   56 H                                  Z Score = 8.29
```

FIG. 1C

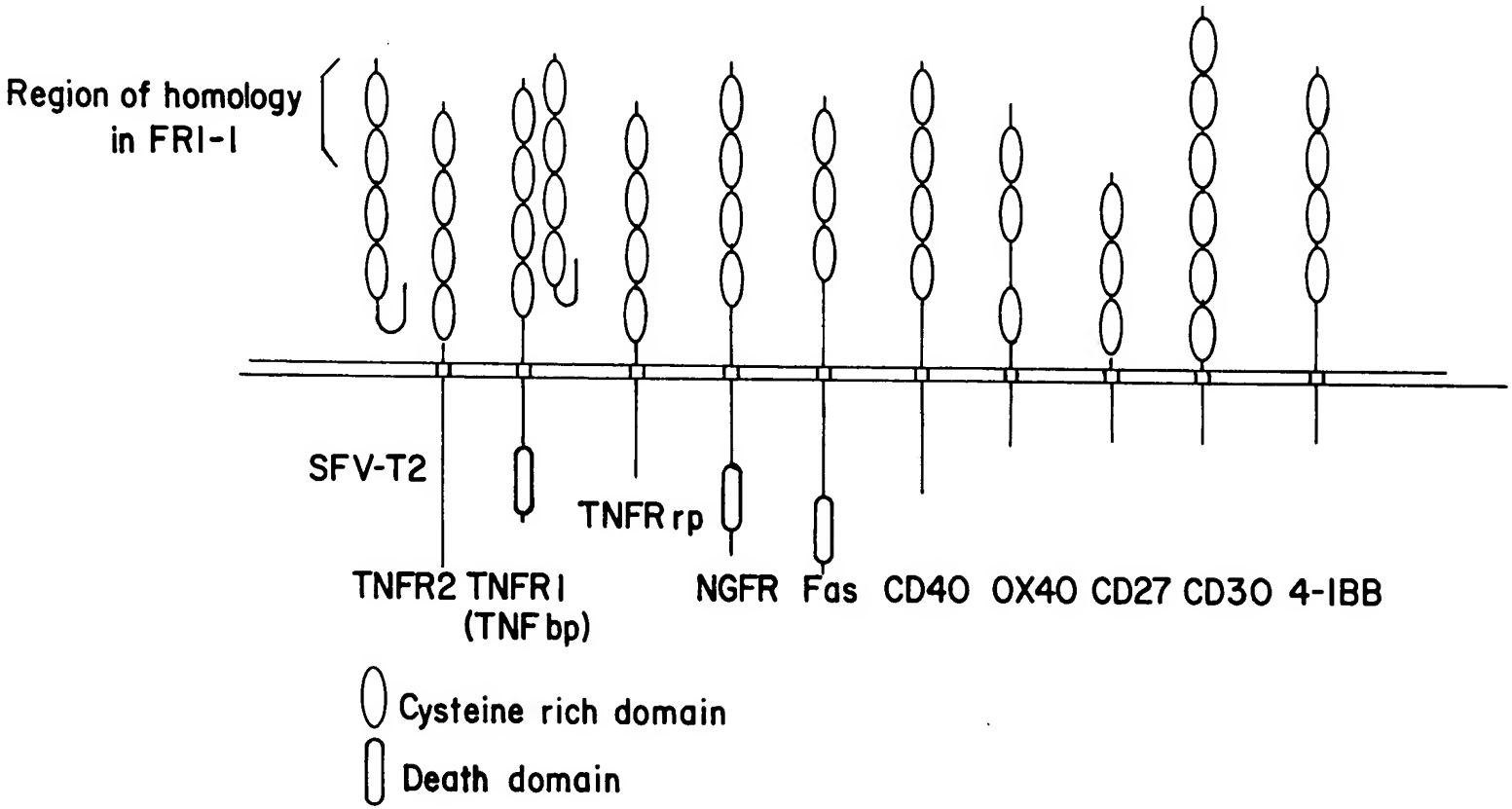
Region of homology
in FRI-I
SFV-T2
TNFR rp
TNFR2
TNFR I
(TNF bp)
NGFR
Fas
CD40
OX40
CD27
CD30
4-IBB
Cysteine rich domain
Death domain

FIG.2A

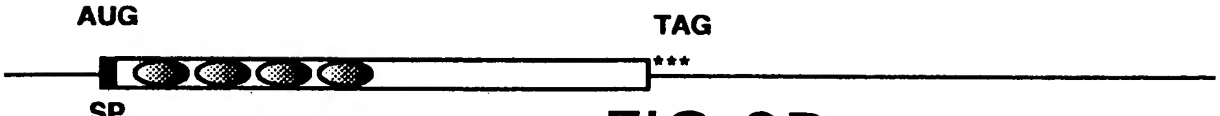

FIG.2B

```
        10                  30                  50
ATCAAAGGCAGGGCATACTTCCTGTTGCCCAGACCTTATATAAAACGTCATGTTCGCCTG
        70                  90                  110
GGCAGCAGAGAAGCACCTAGCACTGGCCCAGCGGCTGCCGCCTGAGGTTTCCAGAGGACC
        130                 150                 170
ACAATGAACAAGTGGCTGTGCTGTGCACTCCTGGTGTTCTTGGACATCATTGAATGGACA
   M  N  K  W  L  C  C  A  L  L  V  F  L  D  I  I  E  W  T
        190                 210                 230
ACCCAGGAAACCTTTCCTCCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTC
T  Q  E  T  F  P  P  K  Y  L  H  Y  D  P  E  T  G  R  Q  L
        250                 270                 290
TTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAG
L  C  D  K  C  A  P  G  T  Y  L  K  Q  H  C  T  V  R  R  K
        310                 330                 350
ACACTGTGTGTCCCTTGCCCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAA
T  L  C  V  P  C  P  D  Y  S  Y  T  D  S  W  H  T  S  D  E
        370                 390                 410
TGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGC
C  V  Y  C  S  P  V  C  K  E  L  Q  T  V  K  Q  E  C  N  R
        430                 450                 470
ACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTG
T  H  N  R  V  C  E  C  E  E  G  R  Y  L  E  L  E  F  C  L
        490                 510                 530
AAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAAC
K  H  R  S  C  P  P  G  L  G  V  L  Q  A  G  T  P  E  R  N
        550                 570                 590
ACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCC
T  V  C  K  R  C  P  D  G  F  F  S  G  E  T  S  S  K  A  P
        610                 630                 650
TGTAGGAAACACACCAACTGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCA
C  R  K  H  T  N  C  S  S  L  G  L  L  L  I  Q  K  G  N  A
        670                 690                 710
ACACATGACAATGTATGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTC
T  H  D  N  V  C  S  G  N  R  E  A  T  Q  N  C  G  I  D  V
        730                 750                 770
ACCCTGTGCGAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGG
T  L  C  E  E  A  F  F  R  F  A  V  P  T  K  I  I  P  N  W
        790                 810                 830
CTGAGTGTTCTGGTGGACAGTTTGCCTGGGACCAAAGTGAATGCAGAGAGTGTAGAGAGG
L  S  V  L  V  D  S  L  P  G  T  K  V  N  A  E  S  V  E  R
        850                 870                 890
ATAAAACGGAGACACAGCTCGCAAGAGCAAACTTTCCAGCTACTTAAGCTGTGGAAGCAT
I  K  R  R  H  S  S  Q  E  Q  T  F  Q  L  L  K  L  W  K  H
        910                 930                 950
CAAAACAGAGACCAGGAAATGGTGAAGAAGATCATCCAAGACATTGACCTCTGTGAAAGC
Q  N  R  D  Q  E  M  V  K  K  I  I  Q  D  I  D  L  C  E  S
        970                 990                 1010
AGTGTGCAACGGCATATCGGCCACGCGAACCTCACCACAGAGCAGCTCCGCATCTTGATG
S  V  Q  R  H  I  G  H  A  N  L  T  T  E  Q  L  R  I  L  M
```

FIG.2C

```
      1030                      1050                      1070
GAGAGCTTGCCTGGGAAGAAGATCAGCCCAGACGAGATTGAGAGAACGAGAAAGACCTGC
E  S  L  P  G  K  K  I  S  P  D  E  I  E  R  T  R  K  T  C
      1090                      1110                      1130
AAACCCAGCGAGCAGCTCCTGAAGCTACTGAGCTTGTGGAGGATCAAAAATGGAGACCAA
K  P  S  E  Q  L  L  K  L  L  S  L  W  R  I  K  N  G  D  Q
      1150                      1170                      1190
GACACCTTGAAGGGCCTGATGTACGCACTCAAGCACTTGAAAGCATACCACTTTCCCAAA
D  T  L  K  G  L  M  Y  A  L  K  H  L  K  A  Y  H  F  P  K
      1210                      1230                      1250
ACCGTCACCCACAGTCTGAGGAAGACCATCAGGTTCTTGCACAGCTTCACCATGTACCGA
T  V  T  H  S  L  R  K  T  I  R  F  L  H  S  F  T  M  Y  R
      1270                      1290                      1310
TTGTATCAGAAACTCTTTCTAGAAATGATAGGGAATCAGGTTCAATCAGTGAAGATAAGC
L  Y  Q  K  L  F  L  E  M  I  G  N  Q  V  Q  S  V  K  I  S
      1330                      1350                      1370
TGCTTATAGTTAGGAATGGTCACTGGGCTGTTTCTTCAGGATGGGCCAACACTGATGGAG
C  L
      1390                      1410                      1430
CAGATGGCTGCTTCTCCGGCTCTTGAAATGGCAGTTGATTCCTTTCTCATCAGTTGGTGG
      1450                      1470                      1490
GAATGAAGATCCTCCAGCCCAACACACACTGGGGAGTCTGAGTCAGGAGAGTGAGGCA
      1510                      1530                      1550
GGCTATTTGATAATTGTGCAAAGCTGCCAGGTGTACACCTAGAAAGTCAAGCACCCTGAG
      1570                      1590                      1610
AAAGAGGATATTTTTATAACCTCAAACATAGGCCCTTTCCTTCCTCTCCTTATGGATGAG
      1630                      1650                      1670
TACTCAGAAGGCTTCTACTATCTTCTGTGTCATCCCTAGATGAAGGCCTCTTTTATTTAT
      1690                      1710                      1730
TTTTTTATTCTTTTTTTCGGAGCTGGGGACCGAACCCAGGGCCTTGCGCTTGCGAGGCAA
      1750                      1770                      1790
GTGCTCTACCACTGAGCTAAATCTCCAACCCCTGAAGGCCTCTTTCTTTCTGCCTCTGAT
      1810                      1830                      1850
AGTCTATGACATTCTTTTTTCTACAATTCGTATCAGGTGCACGAGCCTTATCCCATTTGT
      1870                      1890                      1910
AGGTTTCTAGGCAAGTTGACCGTTAGCTATTTTTCCCTCTGAAGATTTGATTCGAGTTGC
      1930                      1950                      1970
AGACTTGGCTAGACAAGCAGGGGTAGGTTATGGTAGTTTATTTAACAGACTGCCACCAGG
      1990                      2010                      2030
AGTCCAGTGTTTCTTGTTCCTCTGTAGTTGTACCTAAGCTGACTCCAAGTACATTTAGTA
      2050                      2070                      2090
TGAAAAATAATCAACAAATTTTATTCCTTCTATCAACATTGGCTAGCTTTGTTTCAGGGC
      2110                      2130                      2150
ACTAAAAGAAACTACTATATGGAGAAAGAATTGATATTGCCCCCAACGTTCAACAACCCA
      2170                      2190                      2210
ATAGTTTATCCAGCTGTCATGCCTGGTTCAGTGTCTACTGACTATGCGCCCTCTTATTAC
      2230                      2250                      2270
TGCATGCAGTAATTCAACTGGAAATAGTAATAATAATAATAGAAATAAAATCTAGACTCC
      2290                      2310                      2330
ATTGGATCTCTCTGAATATGGGAATATCTAACTTAAGAAGCTTTGAGATTTCAGTTGTGT
      2350                      2370                      2390
TAAAGGCTTTTATTAAAAAGCTGATGCTCTTCTGTAAAAGTTACTAATATATCTGTAAGA
      2410                      2430
CTATTACAGTATTGCTATTTATATCCATCCAG
```

FIG.2D

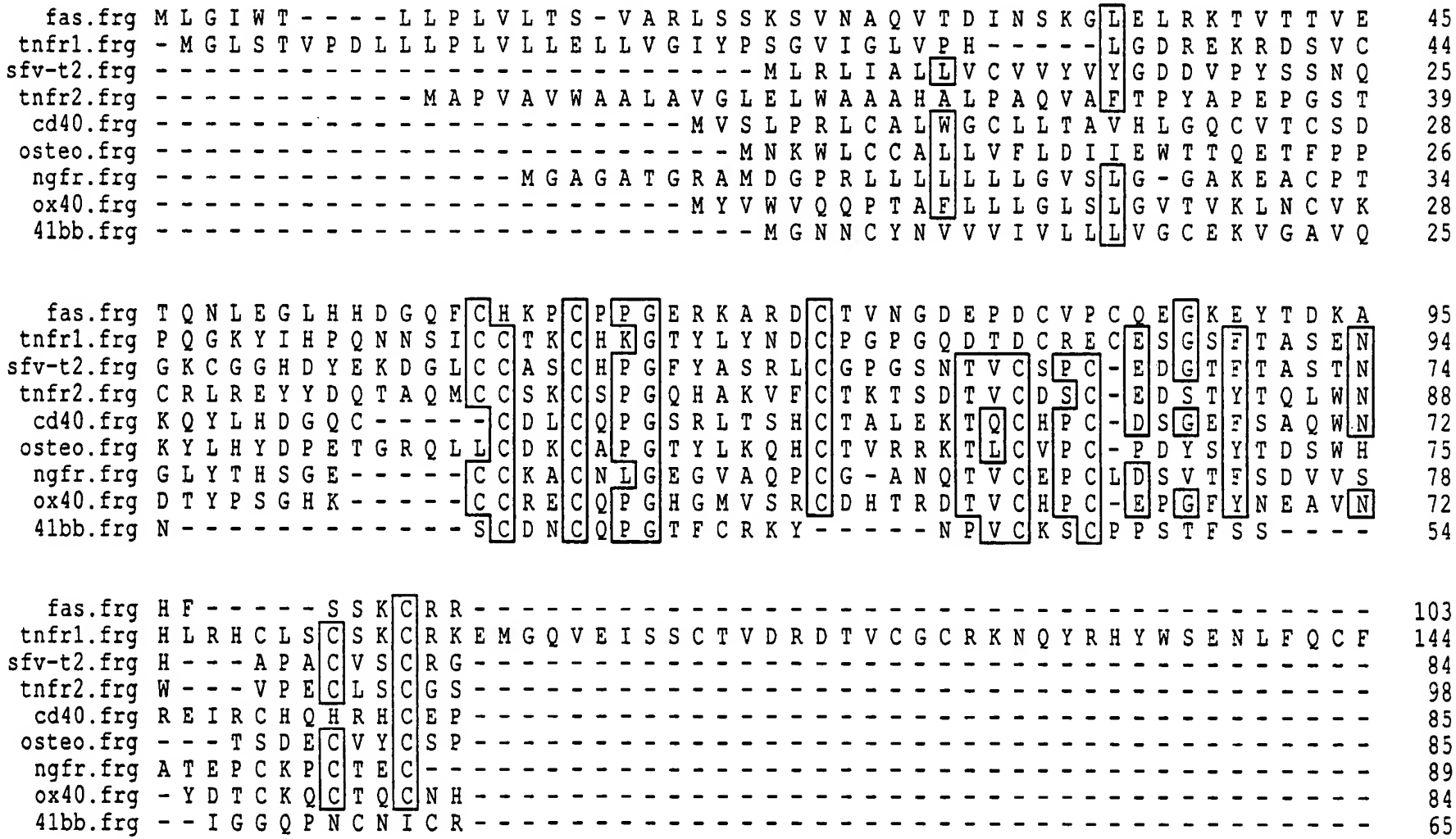

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FIG.2E

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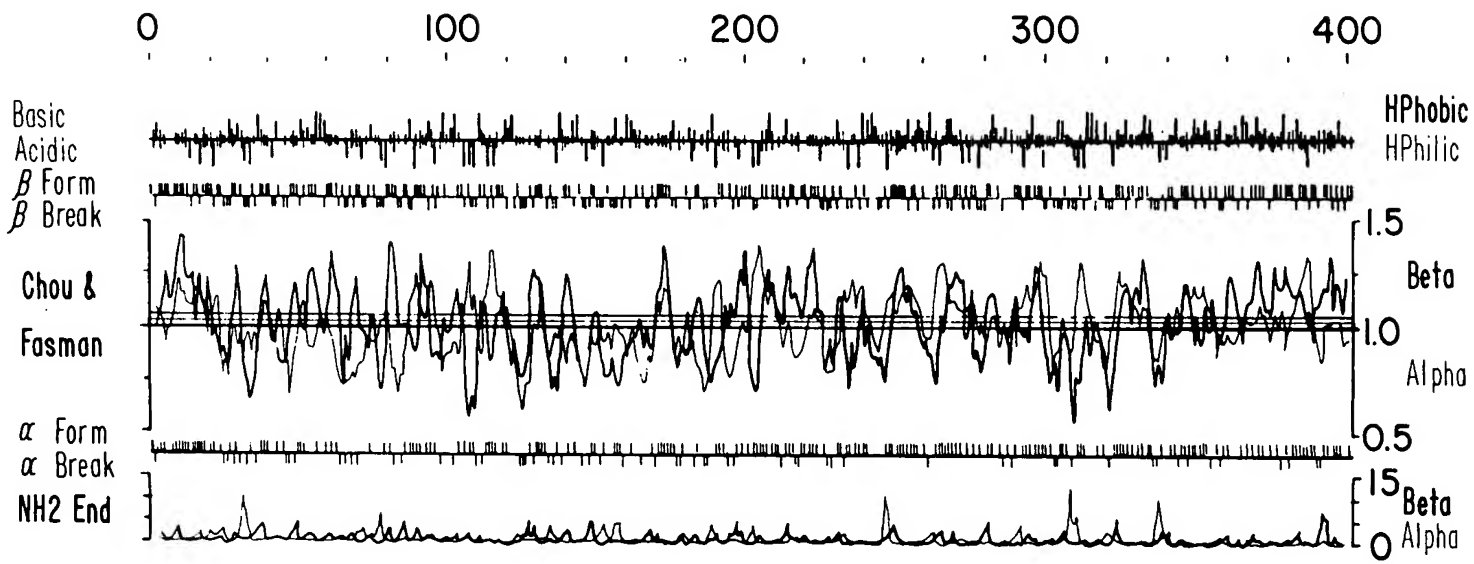
FIG. 3A
FIG. 3B
FIG. 3C
FIG. 3D
FIG. 3E



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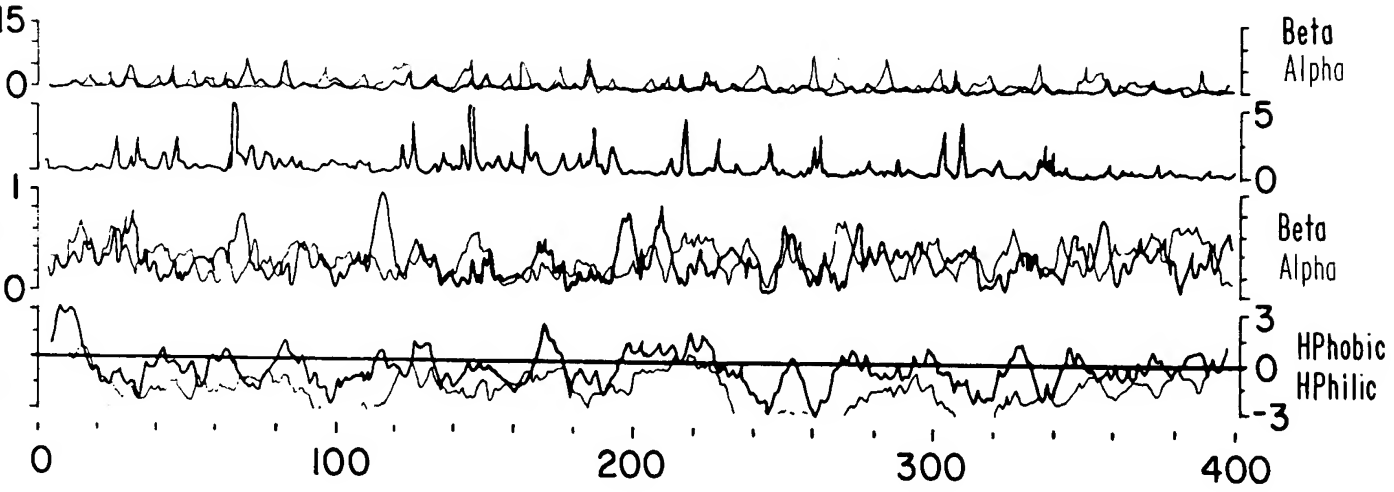
Boyle, *et al.*
USSN: 10/762,159

FIG. 3F

FIG. 3G

FIG. 3H

FIG. 3 I



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Boyle, *et al.*
USSN: 10/762,159

FIG.4A

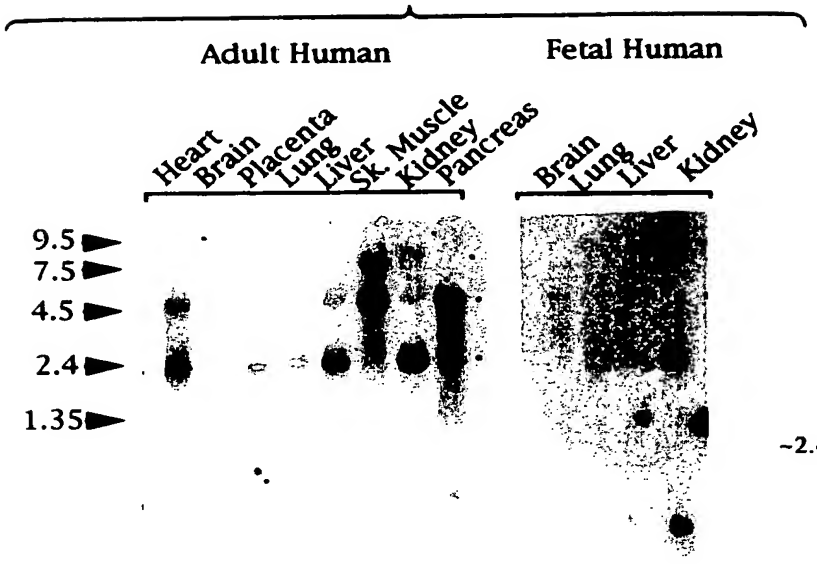
Adult Human
Fetal Human
Heart
Brain
Placenta
Lung
Liver
Sk. Muscle
Kidney
Pancreas
Brain
Lung
Liver
Kidney
9.5
7.5
4.5
2.4
1.35

FIG.4B

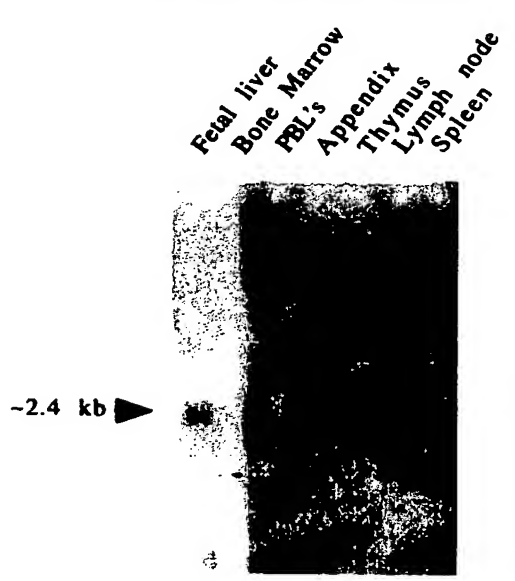
Human Immune System
Fetal liver
Bone Marrow
PBL's
Appendix
Thymus
Lymph node
Spleen
~2.4 kb

FIG.5

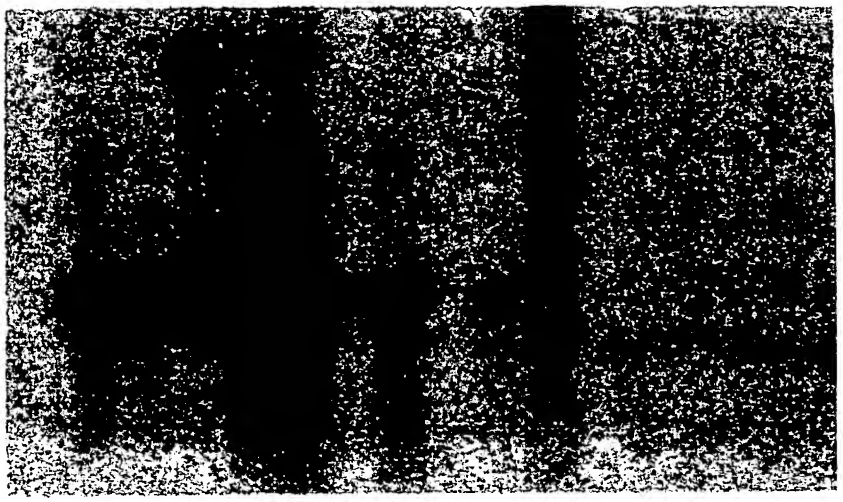
2 11 16 17 22 28 33 38 45 Kb 1 12 18 30
Transgenic Founders
Controls

FIG.6A

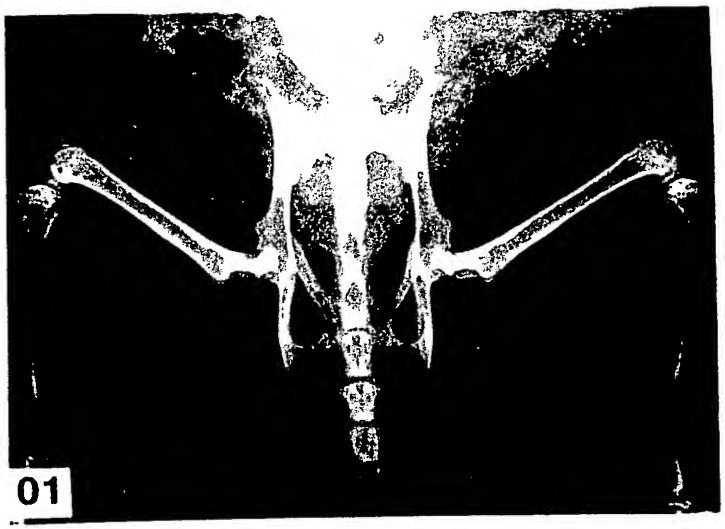

FIG.6B

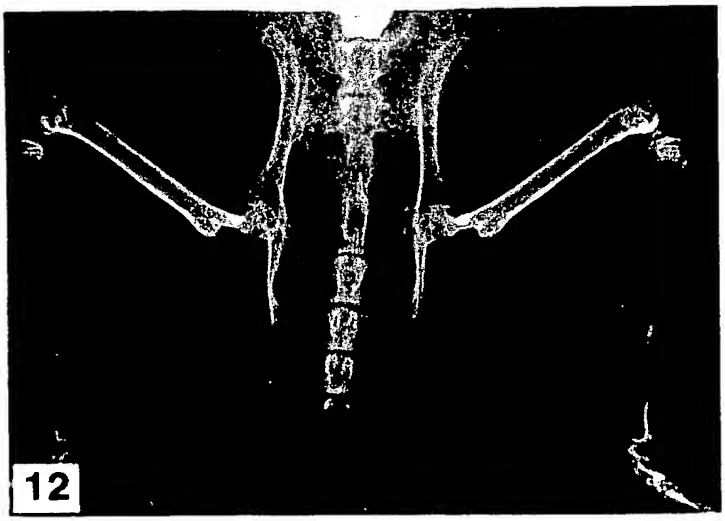

FIG.6C

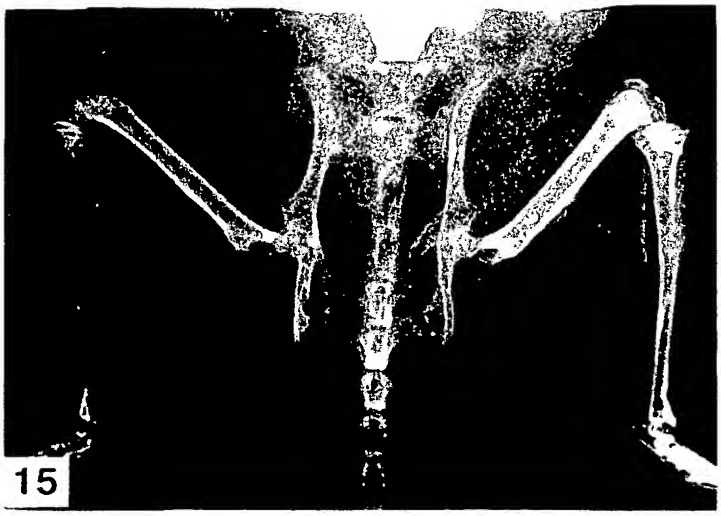

FIG.6D

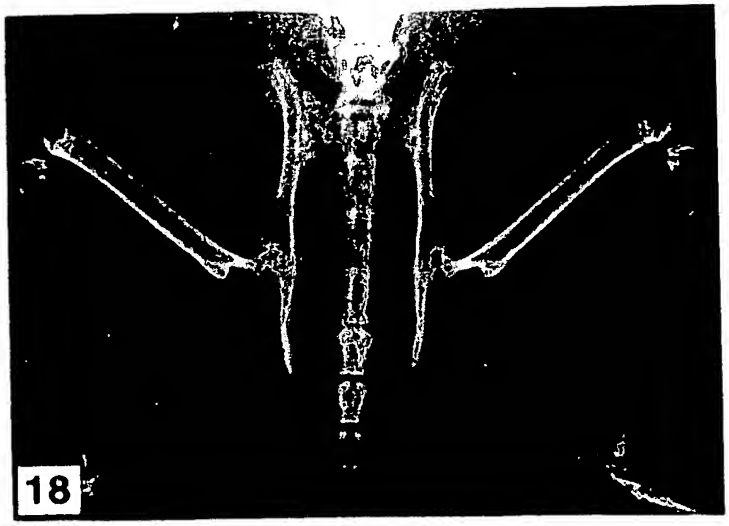

FIG.6E

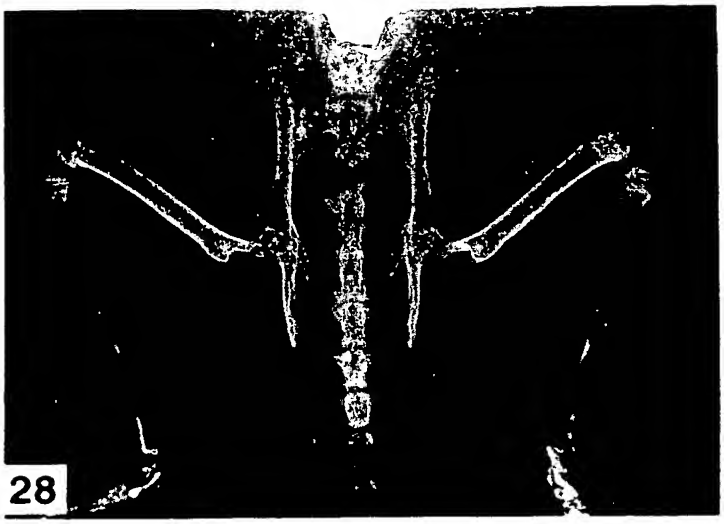

FIG.6F

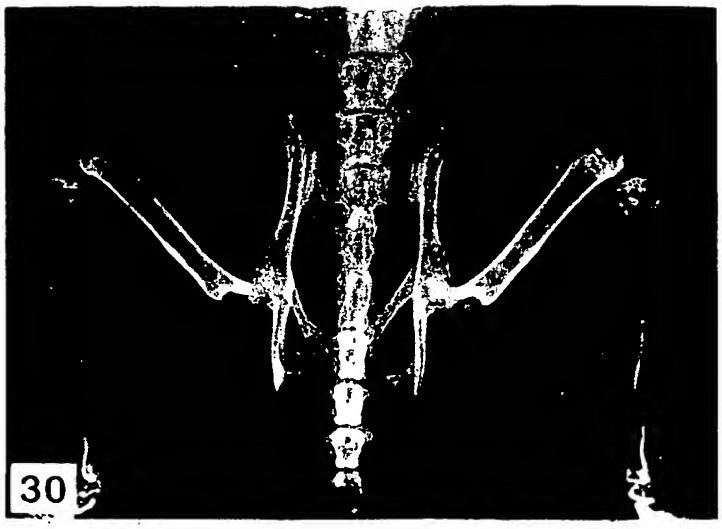

FIG.6G

FIG.6H

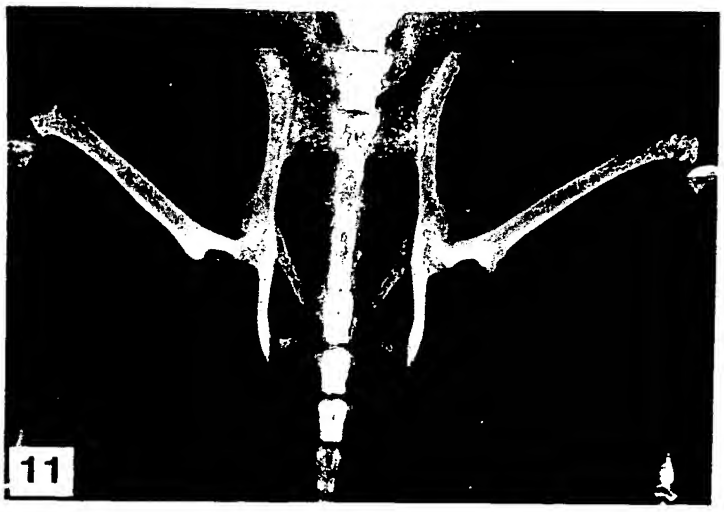

FIG.6I

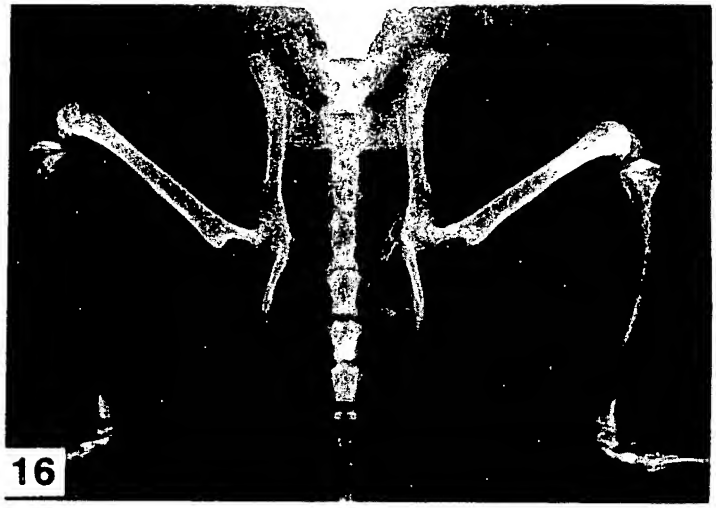

FIG.6J

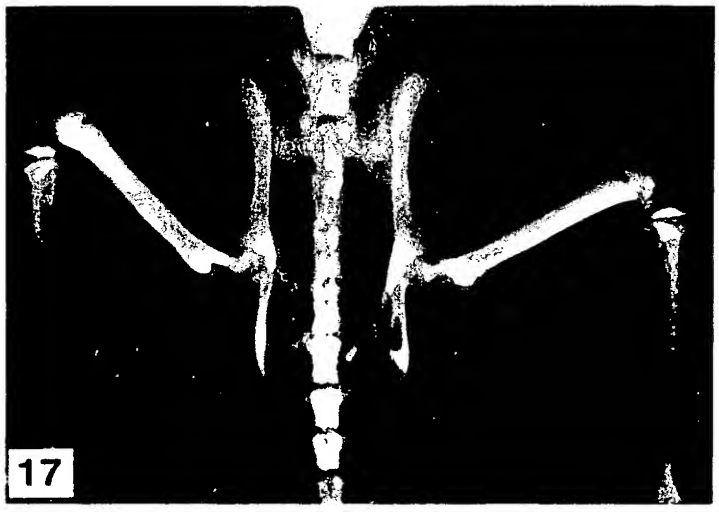

FIG.7A

FIG.7B

FIG.7C

FIG.7D

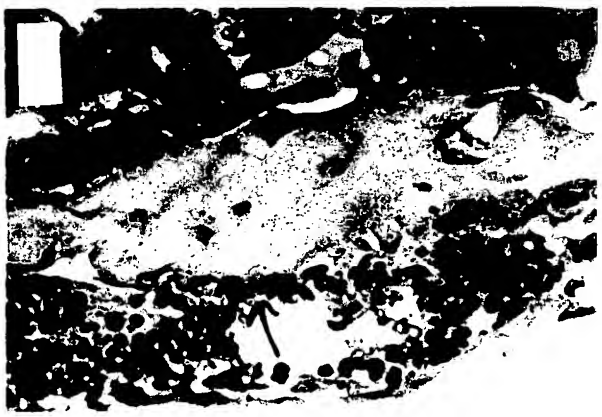

FIG.7E

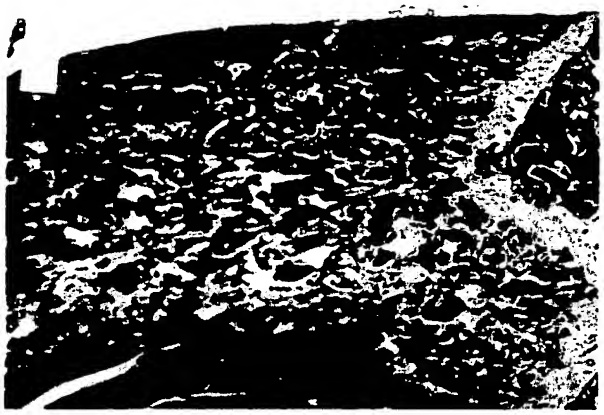

FIG.7F

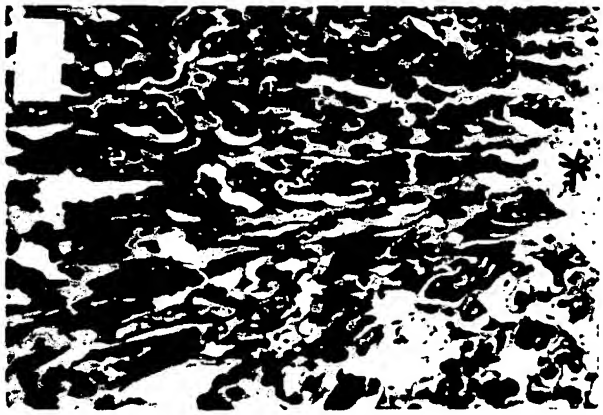

FIG.7G

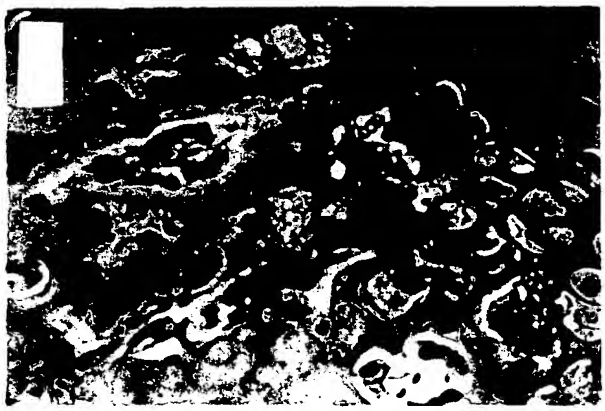

FIG.7H

FIG.8A

FIG.8B

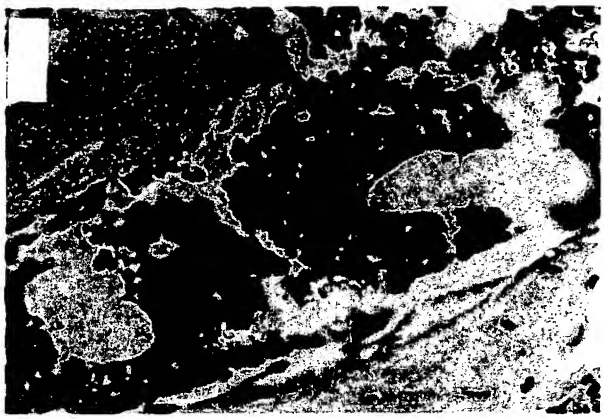

FIG.8C

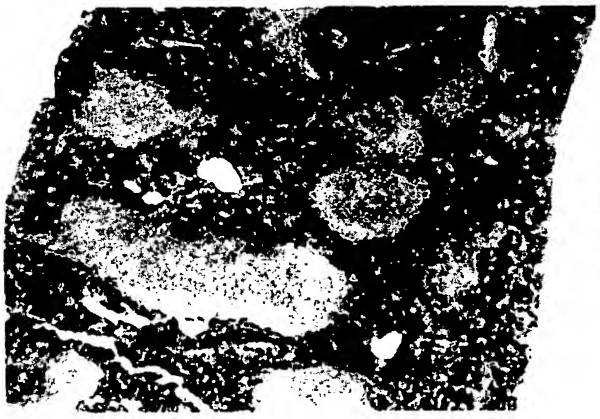

FIG.8D

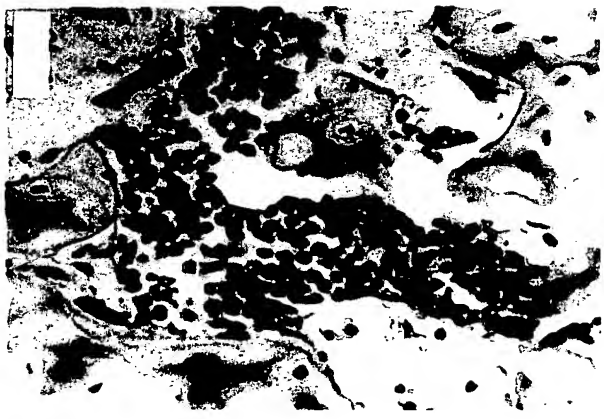

FIG.9A

```
        10                  30                  50
CCTTATATAARACGTCATGATTGCCTGGGCTGCAGAGACGCACCTAGCACTGACCCAGCG
        70                  90                 110
GCTGCCTCCTGAGGTTTCCCGAGGACCACAATGAACAAGTGGCTGTGCTGCGCACTCCTG
                                    M  N  K  W  L  C  C  A  L  L
       130                 150                 170
GTGCTCCTGGACATCATTGAATGGACAACCCAGGAAACCCTTCCTCCAAAGTACTTGCAT
V  L  L  D  I  I  E  W  T  T  Q  E  T  L  P  P  K  Y  L  H
       190                 210                 230
TATGACCCAGAAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTA
Y  D  P  E  T  G  H  Q  L  L  C  D  K  C  A  P  G  T  Y  L
       250                 270                 290
AAACAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTAT
K  Q  H  C  T  V  R  R  K  T  L  C  V  P  C  P  D  H  S  Y
       310                 330                 350
ACGGACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTG
T  D  S  W  H  T  S  D  E  C  V  Y  C  S  P  V  C  K  E  L
       370                 390                 410
CAGTCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGG
Q  S  V  K  Q  E  C  N  R  T  H  N  R  V  C  E  C  E  E  G
       430                 450                 470
CGTTACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTG
R  Y  L  E  I  E  F  C  L  K  H  R  S  C  P  P  G  S  G  V
       490                 510                 530
GTGCAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTC
V  Q  A  G  T  P  E  R  N  T  V  C  K  K  C  P  D  G  F  F
       550                 570                 590
TCAGGTGAGACTTCATCGAAAGCACCCTGTATAAAACACACGAACTGCAGCACATTTGGC
S  G  E  T  S  S  K  A  P  C  I  K  H  T  N  C  S  T  F  G
       610                 630                 650
CTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACAGAGAA
L  L  L  I  Q  K  G  N  A  T  H  D  N  V  C  S  G  N  R  E
       670                 690                 710
GCCACGCAAAAGTGTGGAATAGATGTCACCCTGTGTGAAGAGGCCTTCTTCAGGTTTGCT
A  T  Q  K  C  G  I  D  V  T  L  C  E  E  A  F  F  R  F  A
       730                 750                 770
GTTCCTACCAAGATTATACCAAATTGGCTGAGTGTTTTGGTGGACAGTTTGCCTGGGACC
V  P  T  K  I  I  P  N  W  L  S  V  L  V  D  S  L  P  G  T
```

FIG.9B

```
        790                       810                       830
AAAGTGAATGCCGAGAGTGTAGAGAGGATAAAACGGAGACACAGCTCACAAGAGCAAACC
K  V  N  A  E  S  V  E  R  I  K  R  R  H  S  S  Q  E  Q  T
        850                       870                       890
TTCCAGCTGCTGAAGCTGTGGAAACATCAAAACAGAGACCAGGAAATGGTGAAGAAGATC
F  Q  L  L  K  L  W  K  H  Q  N  R  D  Q  E  M  V  K  K  I
        910                       930                       950
ATCCAAGACATTGACCTCTGTGAAAGCAGCGTGCAGCGGCATCTCGGCCACTCGAACCTC
I  Q  D  I  D  L  C  E  S  S  V  Q  R  H  L  G  H  S  N  L
        970                       990                      1010
ACCACAGAGCAGCTTCTTGCCTTGATGGAGAGCCTGCCTGGGAAGAAGATCAGCCCAGAA
T  T  E  Q  L  L  A  L  M  E  S  L  P  G  K  K  I  S  P  E
       1030                      1050                      1070
GAGATTGAGAGAACGAGAAAGACCTGCAAATCGAGCGAGCAGCTCCTGAAGCTACTCAGT
E  I  E  R  T  R  K  T  C  K  S  S  E  Q  L  L  K  L  L  S
       1090                      1110                      1130
TTATGGAGGATCAAAAATGGTGACCAAGACACCTTGAAGGGCCTGATGTATGCCCTCAAG
L  W  R  I  K  N  G  D  Q  D  T  L  K  G  L  M  Y  A  L  K
       1150                      1170                      1190
CACTTGAAAACATCCCACTTTCCCAAAACTGTCACCCACAGTCTGAGGAAGACCATGAGG
H  L  K  T  S  H  F  P  K  T  V  T  H  S  L  R  K  T  M  R
       1210                      1230                      1250
TTCCTGCACAGCTTCACAATGTACAGACTGTATCAGAAGCTCTTTTTAGAAATGATAGGG
F  L  H  S  F  T  M  Y  R  L  Y  Q  K  L  F  L  E  M  I  G
       1270                      1290                      1310
AATCAGGTTCAATCCGTGAAAATAAGCTGCTTATAACTAGGAATGGTCACTGGGCTGTTT
N  Q  V  Q  S  V  K  I  S  C  L

CTTCA
```

FIG.9C

```
        10                  30                  50
GTATATATAACGTGATGAGCGTACGGGTGCGGAGACGCACCGGAGCGCTCGCCCAGCCGC
        70                  90                 110
CGYCTCCAAGCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTGTGCTGCGCGCT
                                    M  N  K  L  L  C  C  A  L
       130                 150                 170
CGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGTACCT
 V  F  L  D  I  S  I  K  W  T  T  Q  E  T  F  P  P  K  Y  L
       190                 210                 230
TCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTA
 H  Y  D  E  E  T  S  H  Q  L  L  C  D  K  C  P  P  G  T  Y
       250                 270                 290
CCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGCCCTGACCACTA
 L  K  Q  H  C  T  A  K  W  K  T  V  C  A  P  C  P  D  H  Y
       310                 330                 350
CTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGA
 Y  T  D  S  W  H  T  S  D  E  C  L  Y  C  S  P  V  C  K  E
       370                 390                 410
GCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGA
 L  Q  Y  V  K  Q  E  C  N  R  T  H  N  R  V  C  E  C  K  E
       430                 450                 470
AGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCTCCTGGATTTGG
 G  R  Y  L  E  I  E  F  C  L  K  H  R  S  C  P  P  G  F  G
       490                 510                 530
AGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGTCCAGATGGGTT
 V  V  Q  A  G  T  P  E  R  N  T  V  C  K  R  C  P  D  G  F
       550                 570                 590
CTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAATTGCAGTGTCTT
 F  S  N  E  T  S  S  K  A  P  C  R  K  H  T  N  C  S  V  F
       610                 630                 650
TGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAG
 G  L  L  L  T  Q  K  G  N  A  T  H  D  N  I  C  S  G  N  S
       670                 690                 710
TGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCATTCTTCAGGTT
 E  S  T  Q  K  C  G  I  D  V  T  L  C  E  E  A  F  F  R  F
       730                 750                 770
TGCTGTTCCTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGG
 A  V  P  T  K  F  T  P  N  W  L  S  V  L  V  D  N  L  P  G
```

FIG.9D

```
        790                   810                   830
CACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCACAAGAACA
 T  K  V  N  A  E  S  V  E  R  I  K  R  Q  H  S  S  Q  E  Q
        850                   870                   890
GACTTTCCAGCTGCTGAAGTTATGGAAACATCAAAACAAAGACCAAGATATAGTCAAGAA
 T  F  Q  L  L  K  L  W  K  H  Q  N  K  D  Q  D  I  V  K  K
        910                   930                   950
GATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACATGCTAA
 I  I  Q  D  I  D  L  C  E  N  S  V  Q  R  H  I  G  H  A  N
        970                   990                  1010
CCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGAGC
 L  T  F  E  Q  L  R  S  L  M  E  S  L  P  G  K  K  V  G  A
       1030                  1050                  1070
AGAAGACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCT
 E  D  I  E  K  T  I  K  A  C  K  P  S  D  Q  I  L  K  L  L
       1090                  1110                  1130
CAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTAATGCACGCACT
 S  L  W  R  I  K  N  G  D  Q  D  T  L  K  G  L  M  H  A  L
       1150                  1170                  1190
AAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTAAAGAAGACCAT
 K  H  S  K  T  Y  H  F  P  K  T  V  T  Q  S  L  K  K  T  I
       1210                  1230                  1250
CAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTTAGAAATGAT
 R  F  L  H  S  F  T  M  Y  K  L  Y  Q  K  L  F  L  E  M  I
       1270                  1290                  1310
AGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATGGCCATTGAGCT
 G  N  Q  V  Q  S  V  K  I  S  C  L
       1330                  1350
GTTTCCTCACAATTGGCGAGATCCCATGGATGATAA
```

FIG.9E

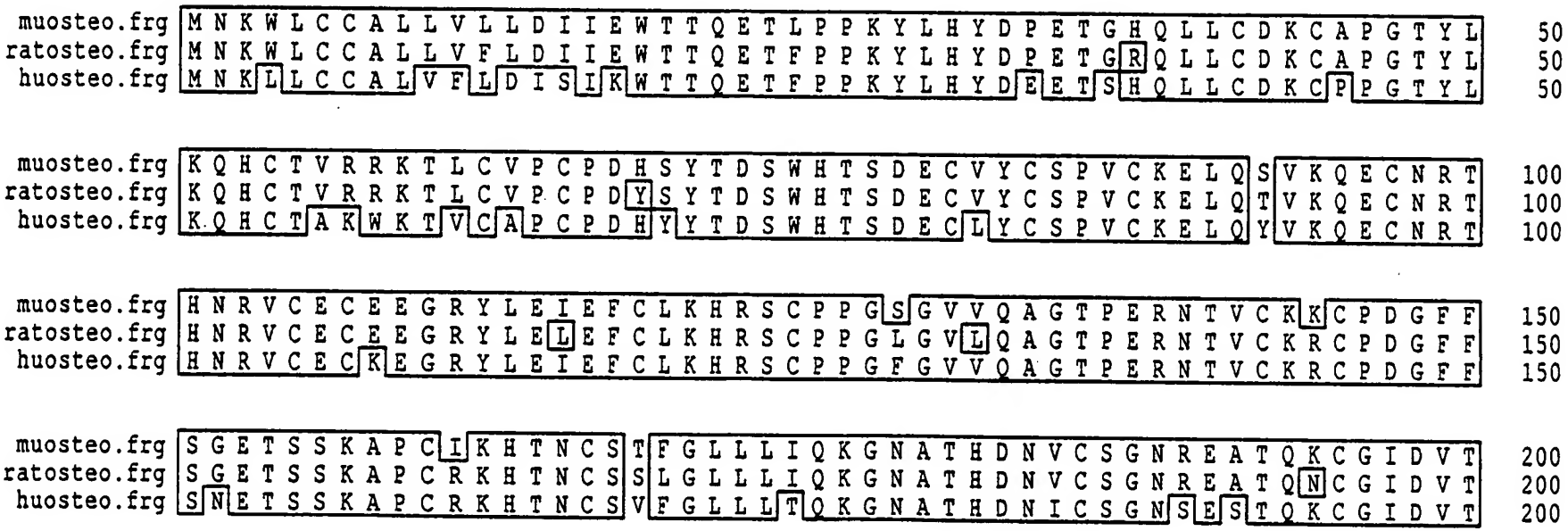

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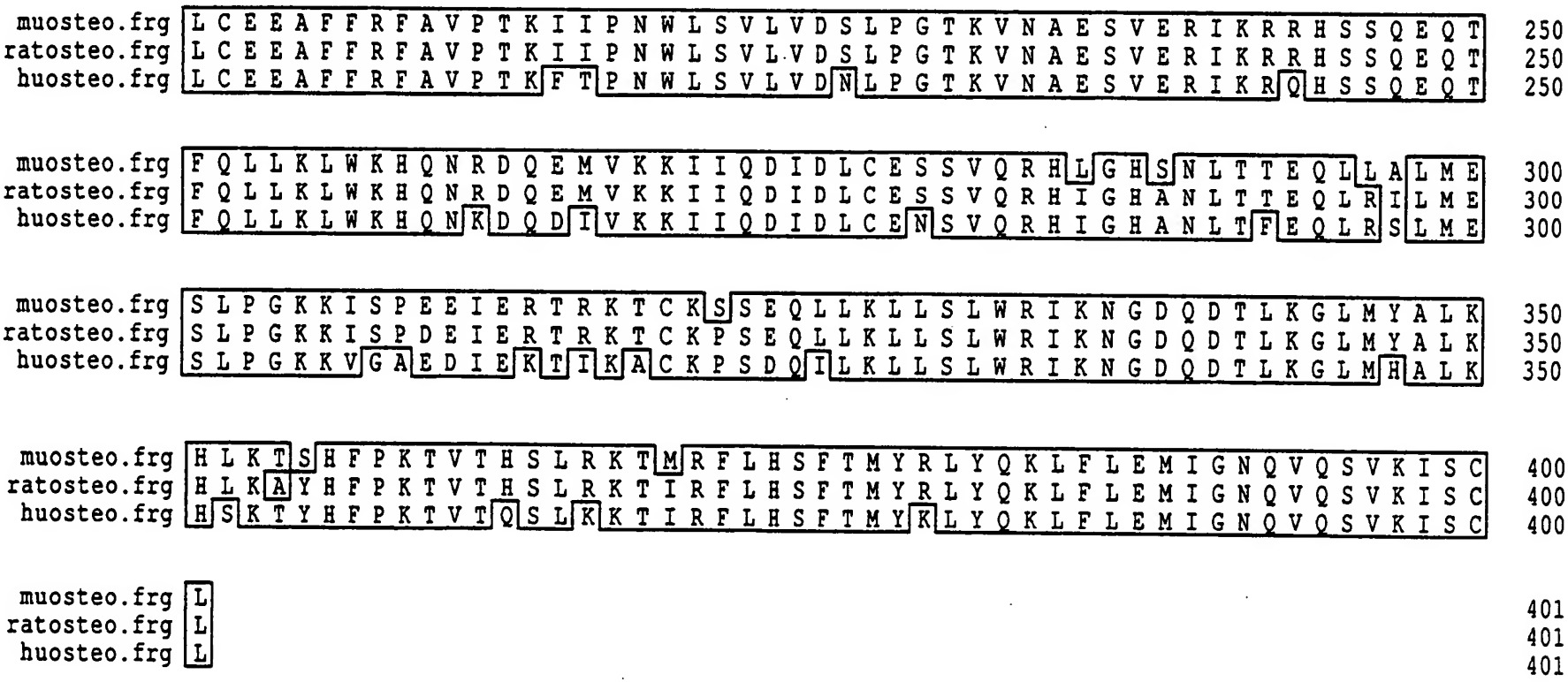
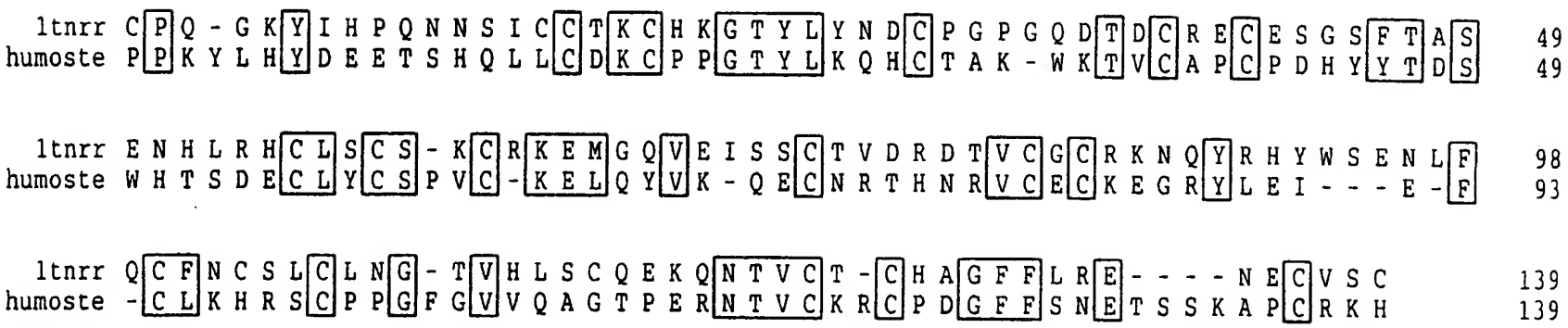
FIG.9F



OSTEOPROTEGERIN
Boyle, *et al.*
USSN: 10/762,159

FIG. 10



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Boyle, *et al.*
USSN: 10/762,159

FIG. 11

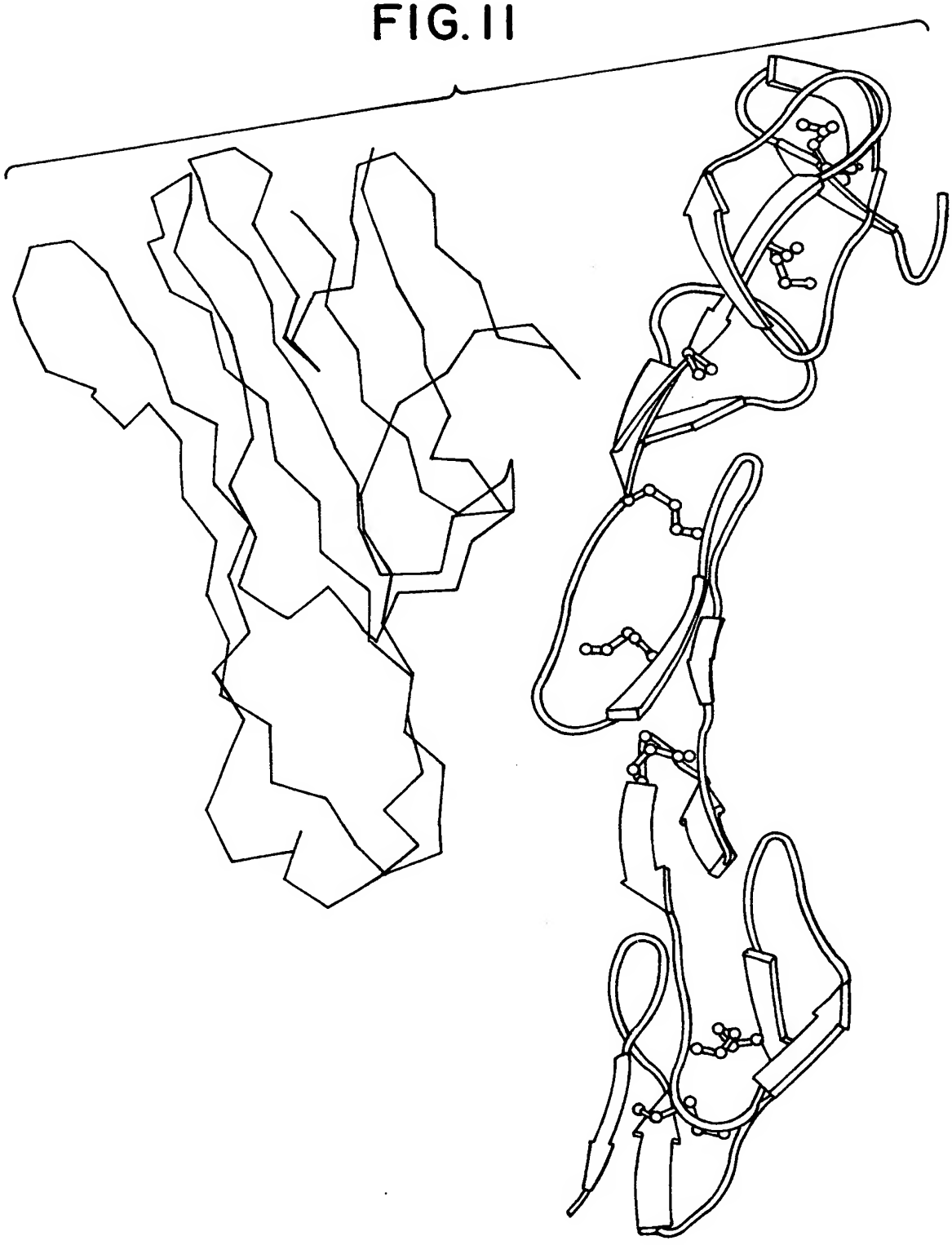
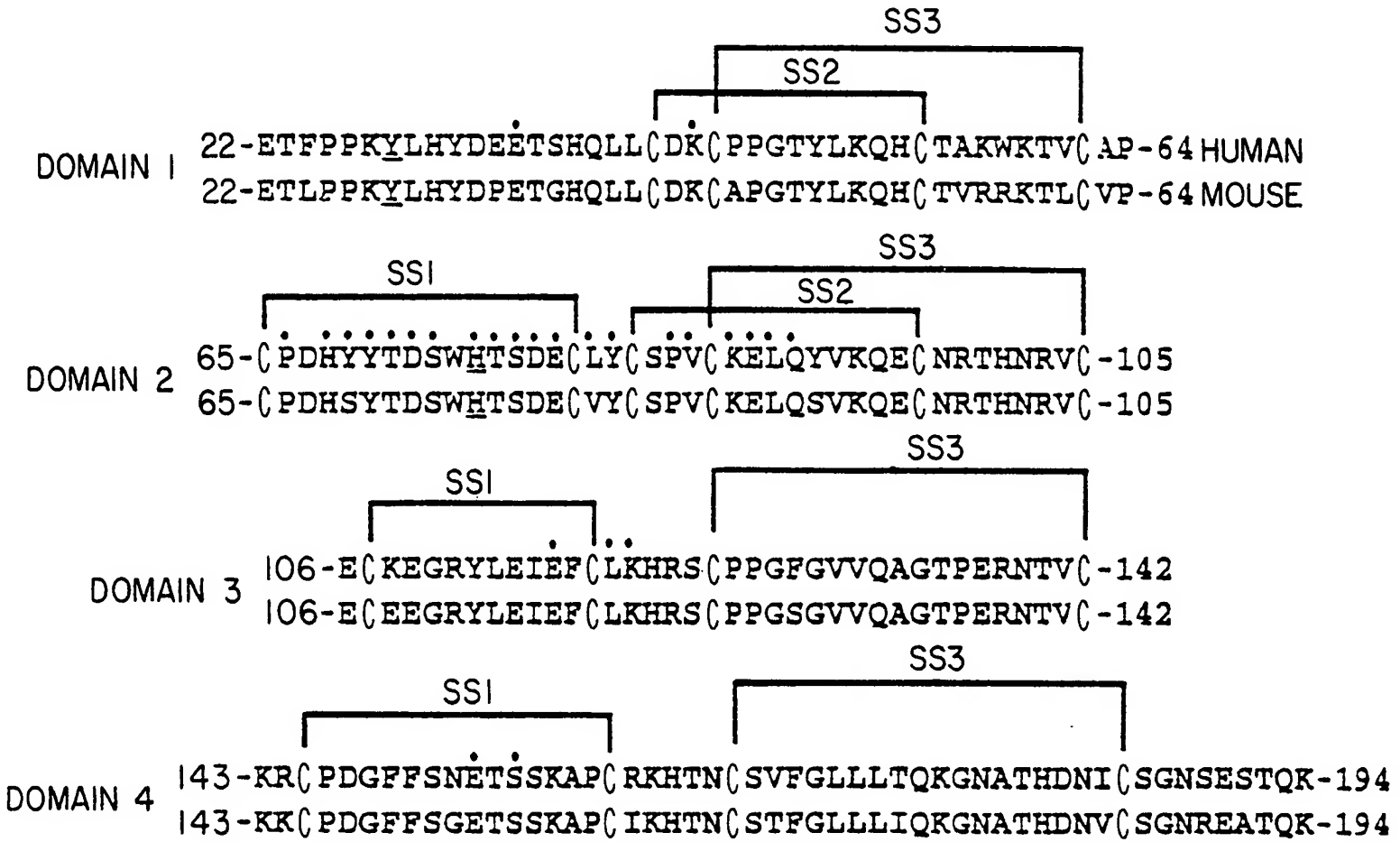


FIG. 12A



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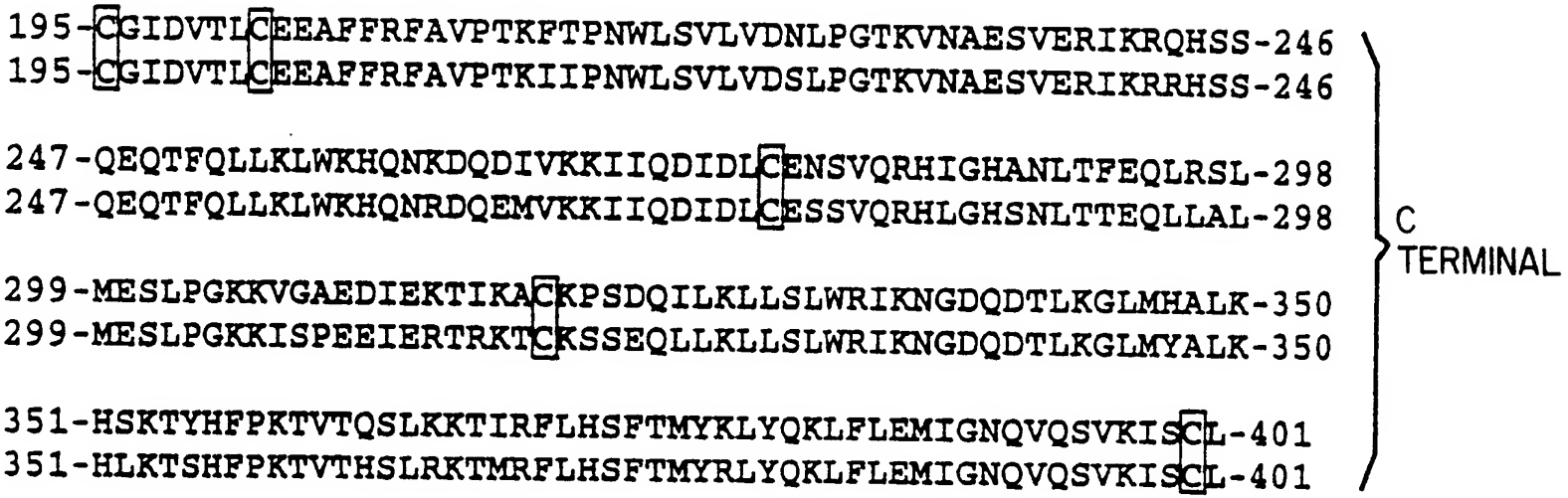
Boyle, *et al.*
USSN: 10/762,159

FIG.12B



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Boyle, *et al.*
USSN: 10/762,159

FIG.13A

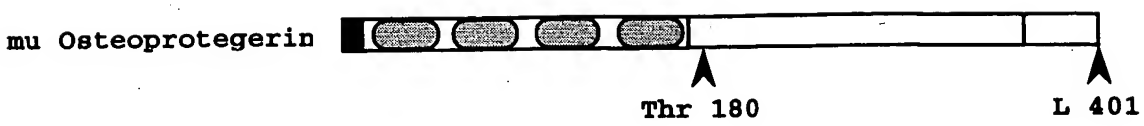


FIG.13B

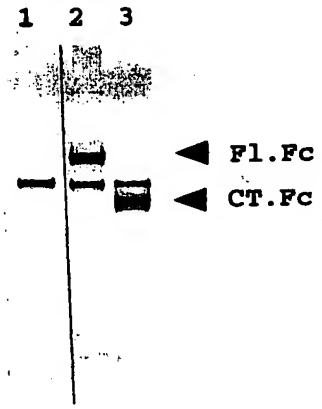


FIG.13C

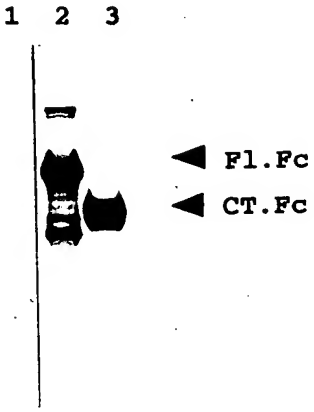


FIG.14A

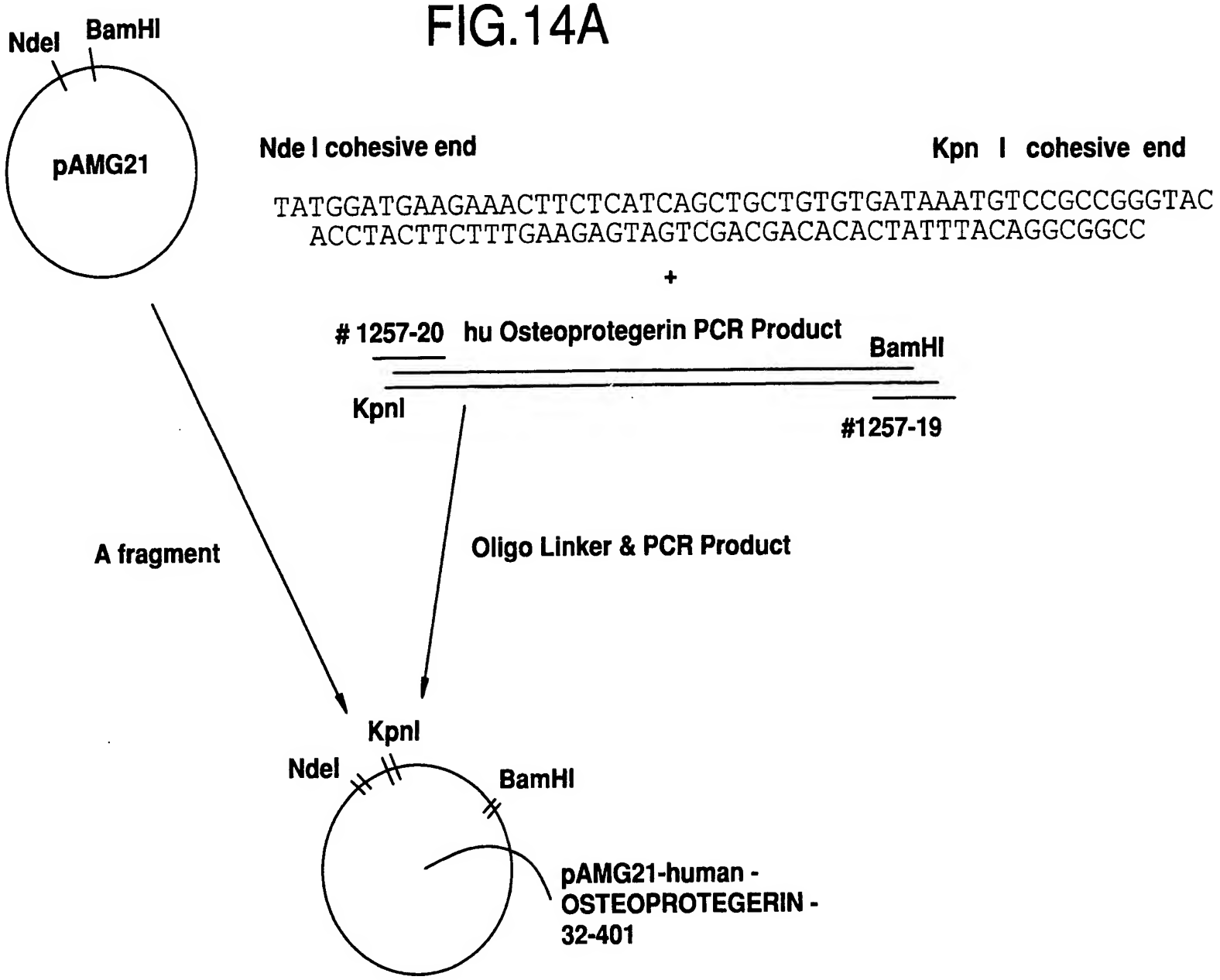

NdeI
BamHI
pAMG21
Nde I cohesive end
Kpn I cohesive end
TATGGATGAAGAAACTTCTCATCAGCTGCTGTGTGATAAATGTCCGCCGGGTAC
ACCTACTTCTTTGAAGAGTAGTCGACGACACACTATTTACAGGCGGCC
+
1257-20 hu Osteoprotegerin PCR Product
BamHI
KpnI
#1257-19
A fragment
Oligo Linker & PCR Product
KpnI
NdeI
BamHI
pAMG21-human -
OSTEOPROTEGERIN -
32-401

FIG. 14B

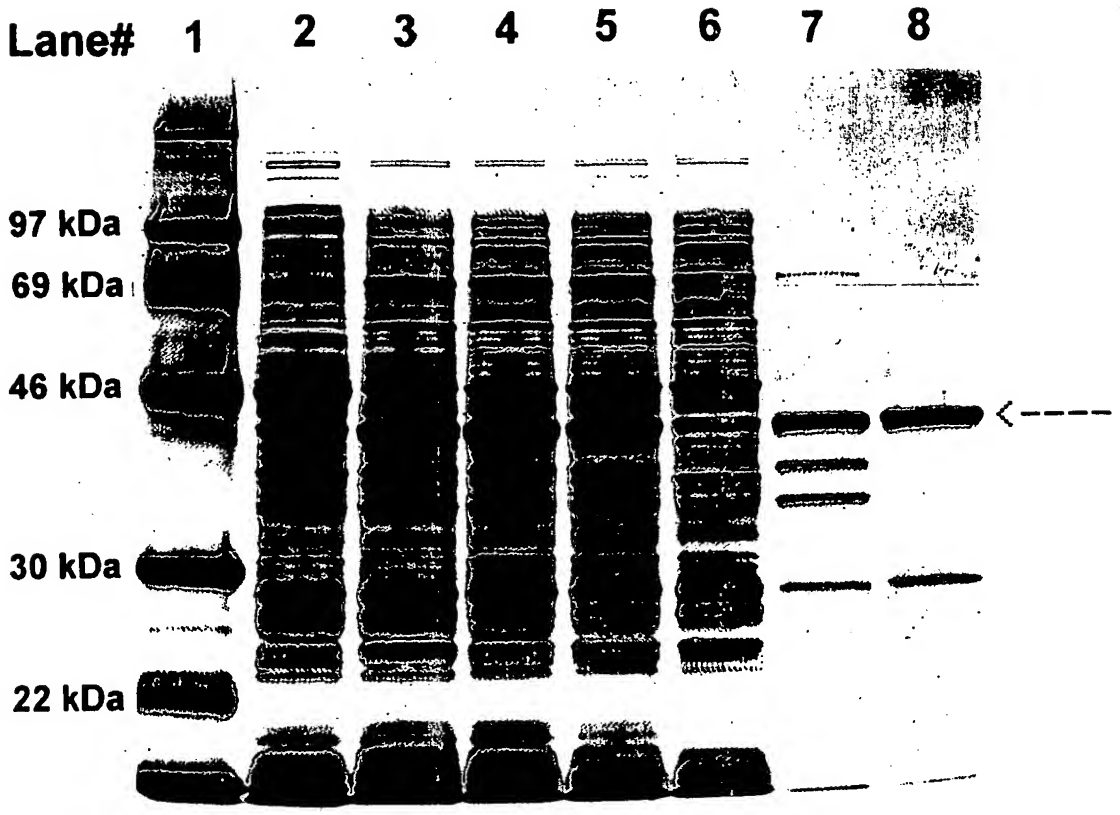


FIG.15

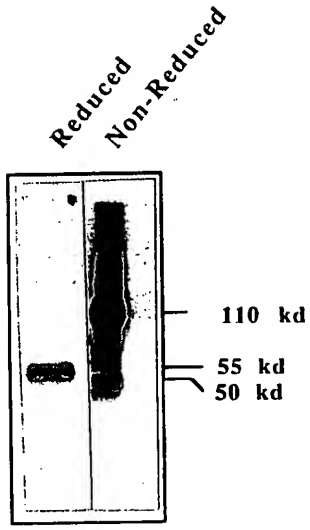


FIG.16A

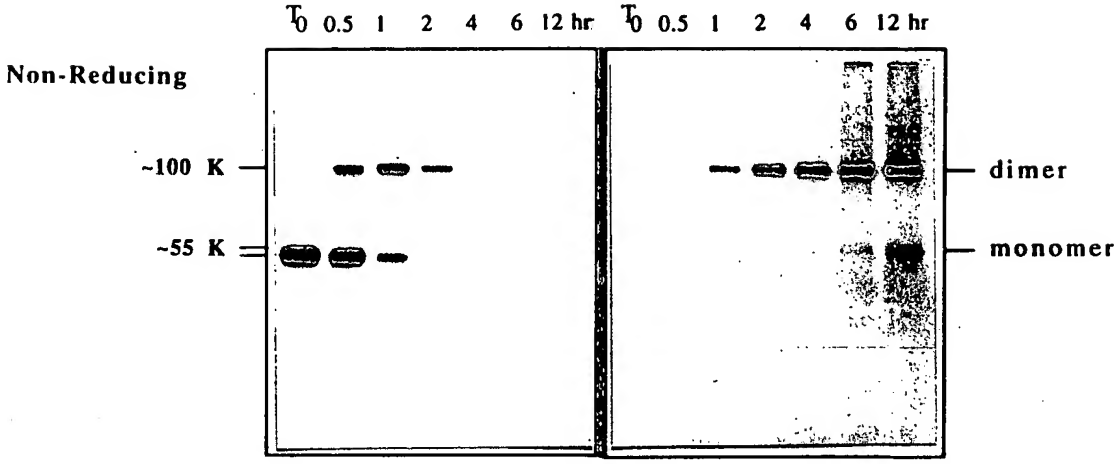


FIG.16B

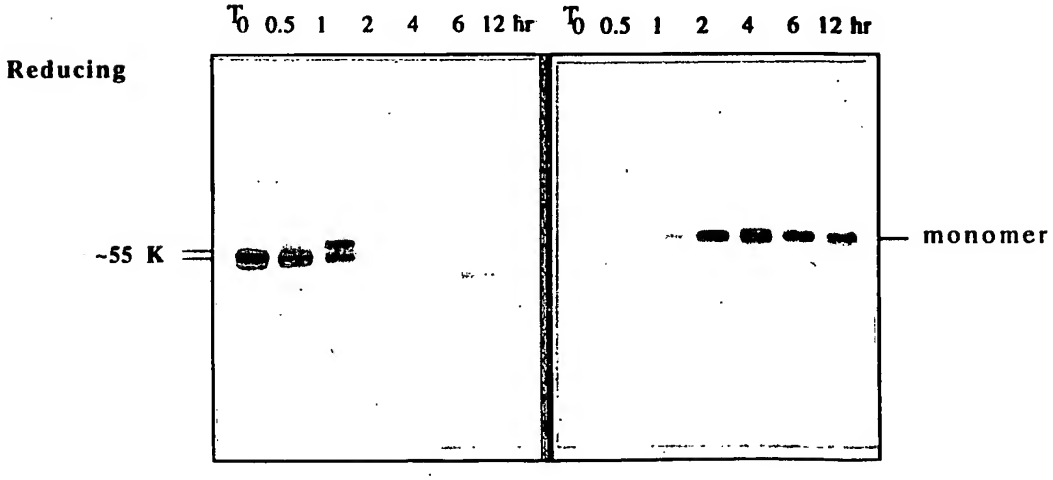


FIG. 17

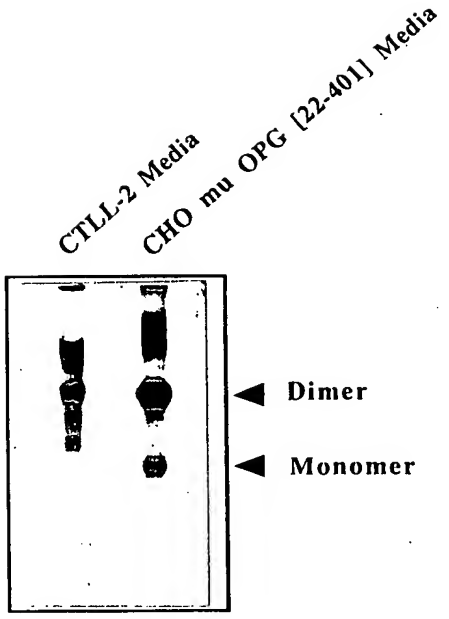
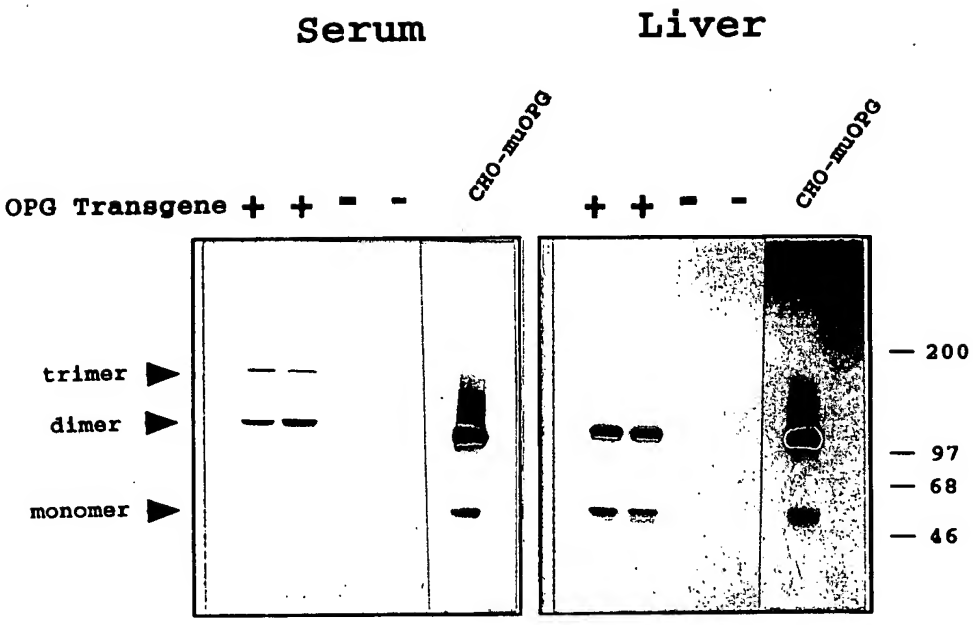


FIG. 18


Serum
Liver
CHO-muOPG
CHO-muOPG
OPG Transgene + + - -
+ + - -
trimer
dimer
monomer
200
97
68
46

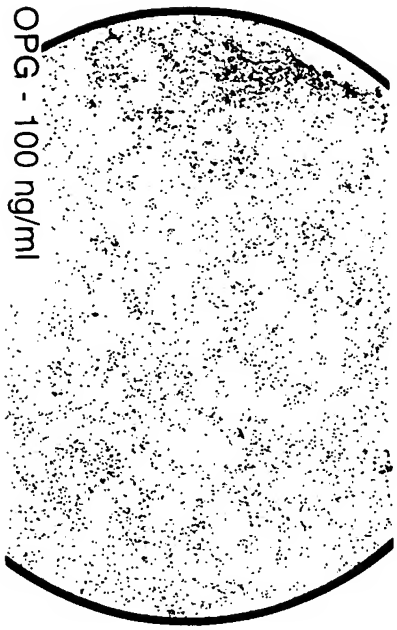


FIG.19A

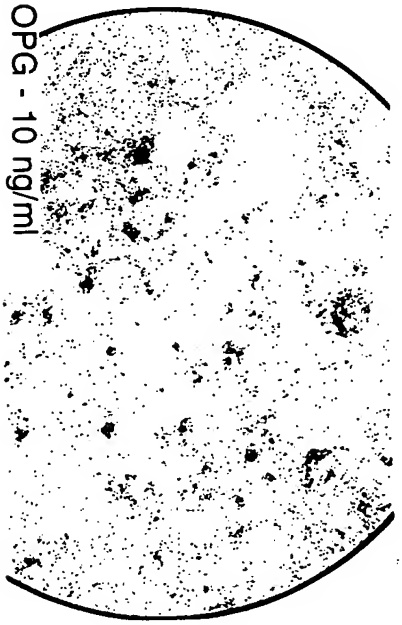


FIG.19B

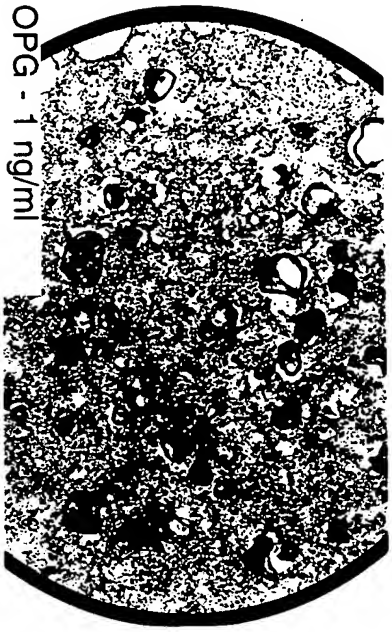


FIG.19C

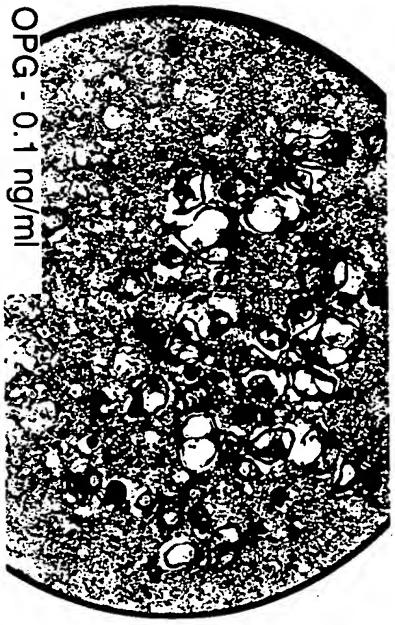


FIG.19D

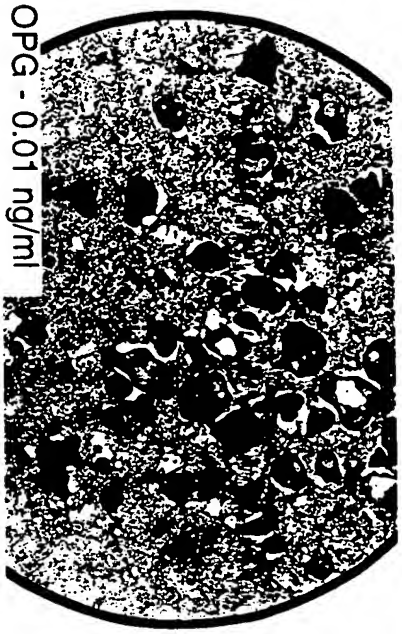


FIG.19E

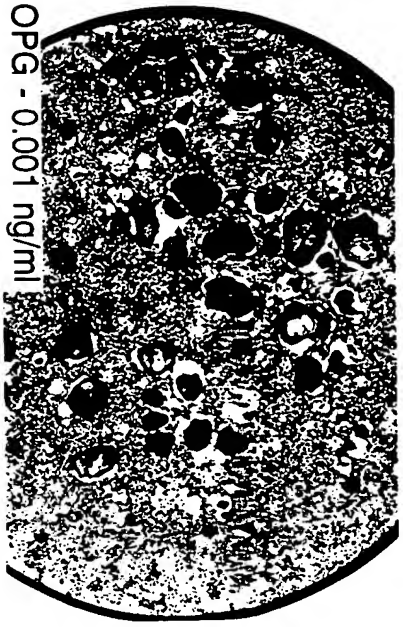


FIG.19F

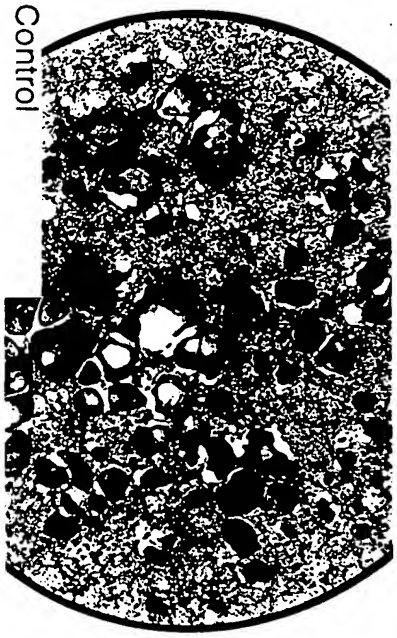


FIG.19G

FIG.20

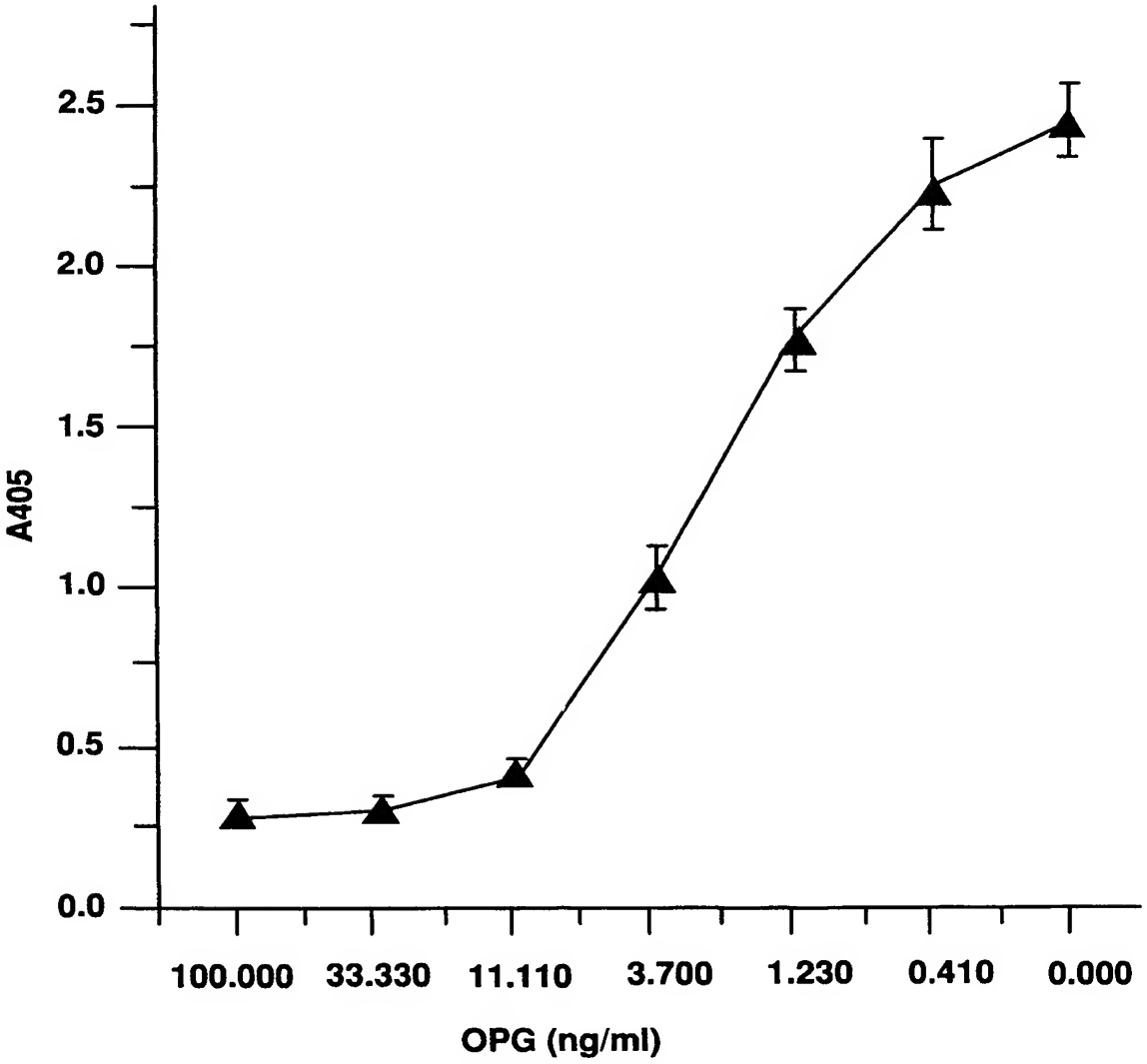
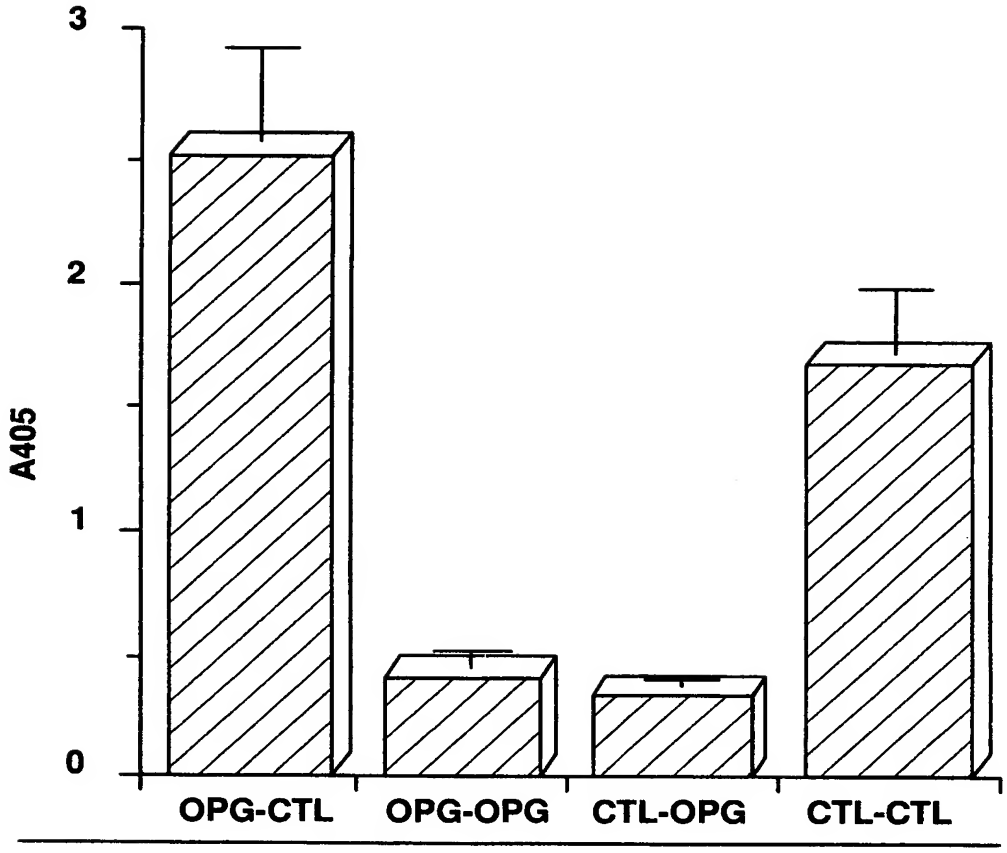

2.5
2.0
1.5
1.0
0.5
0.0
A405
100.000
33.330
11.110
3.700
1.230
0.410
0.000
OPG (ng/ml)

FIG.21



Legend

Growth	Intermediate	Terminal
Bone marrow cells CSF -1	PGE2 + CSF-1	ST2 cells 1,25 (OH)2 D3 Dexamethasone

4 days	2 days	8 - 10 days

Groups	OPG	OPG
CTL - CTL	– – –	– – –
OPG - CTL	100 ng/ml	– – –
OPG - OPG	– – –	100 ng/ml
OPG - OPG	100 ng/ml	100 ng/ml

FIG.22A

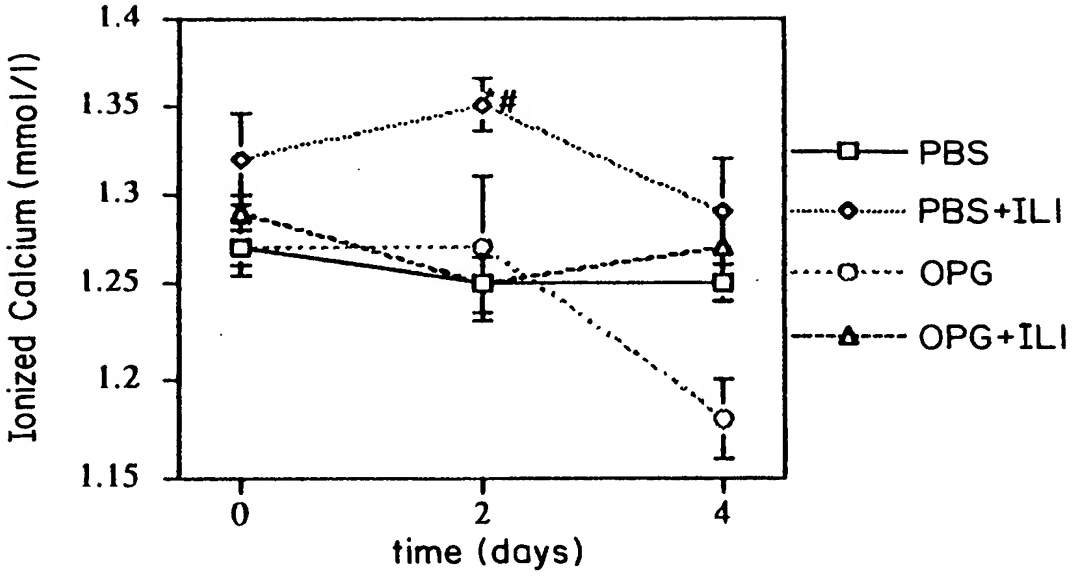
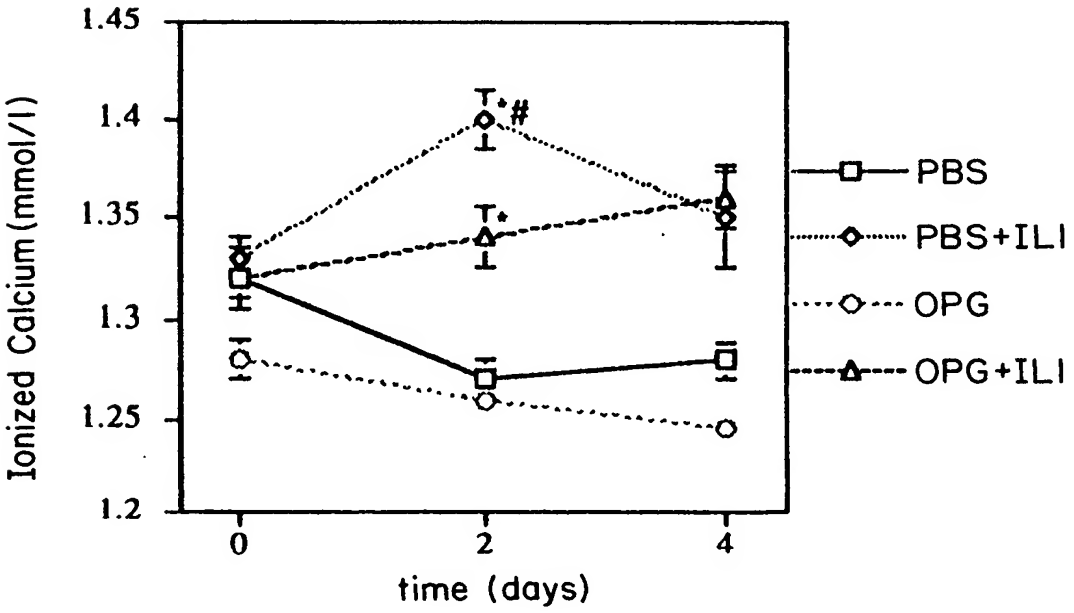


FIG.22B



* Different to PBS, $p < 0.05$
# Different to OPG + IL1, $p < 0.05$

FIG.23A

PBS/PBS

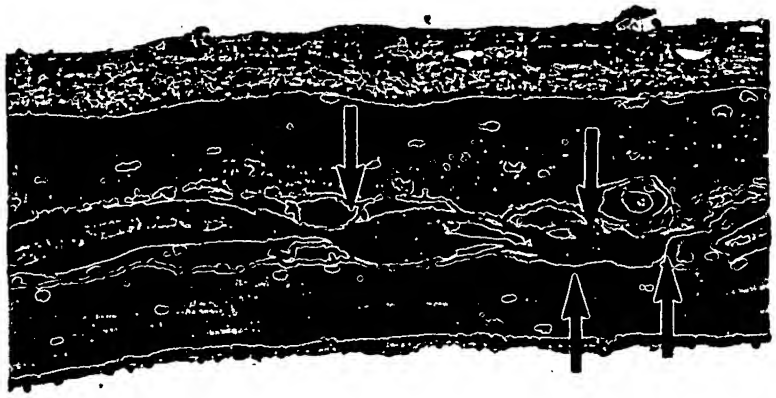
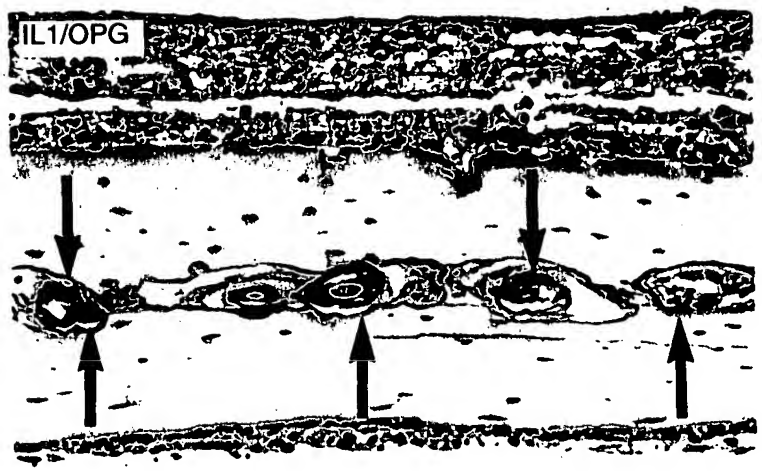


FIG.23B

FIG.23C

FIG.23D



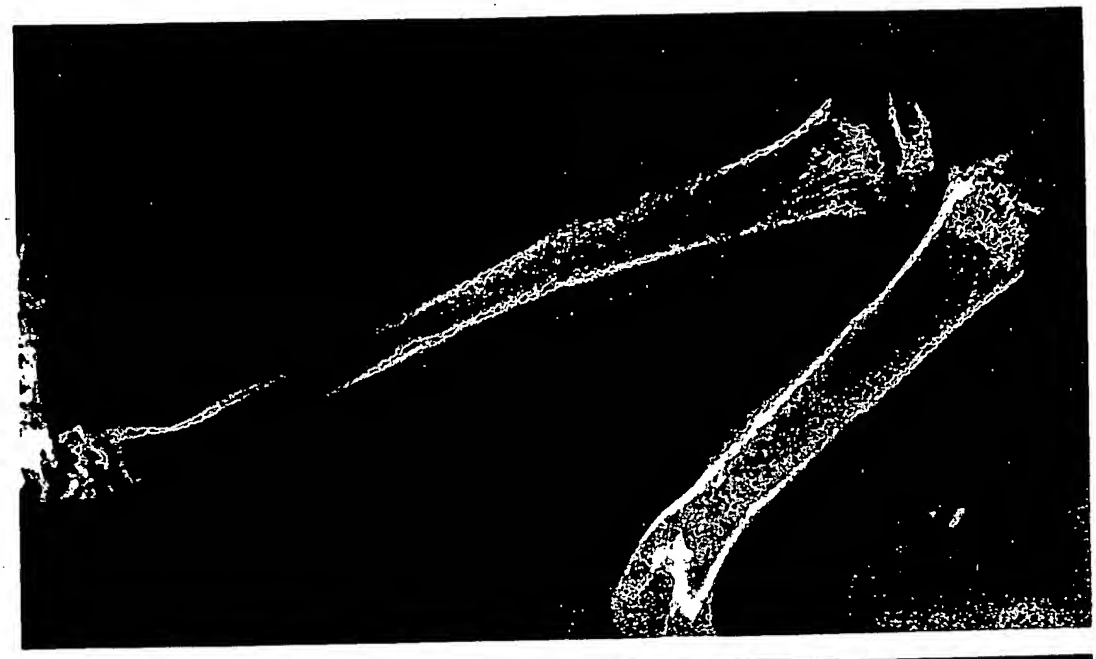


FIG.24A

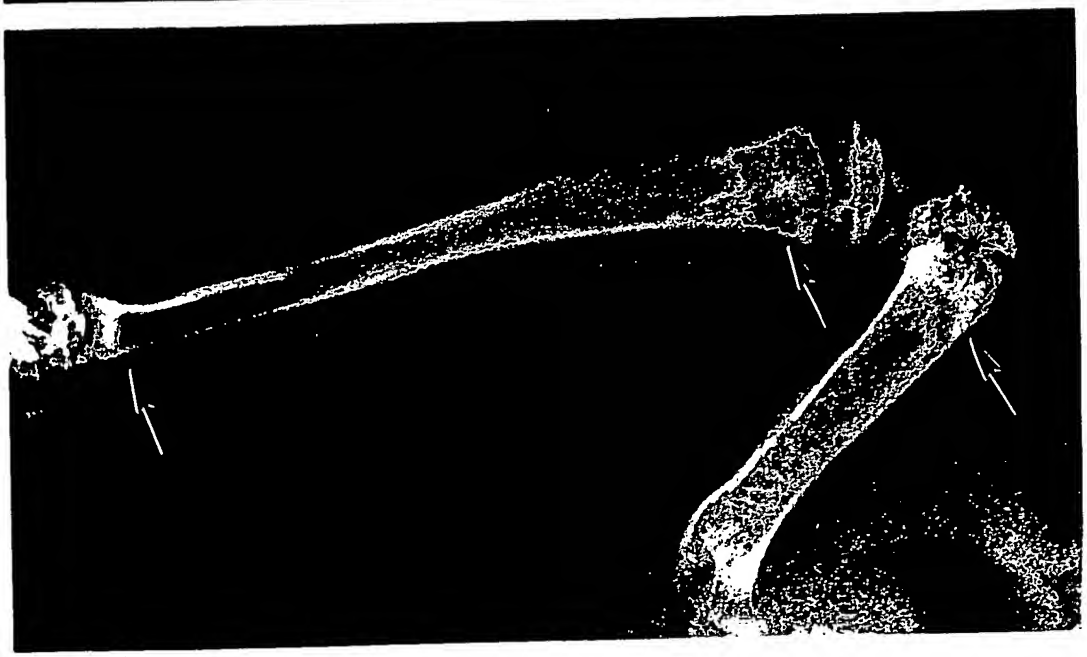
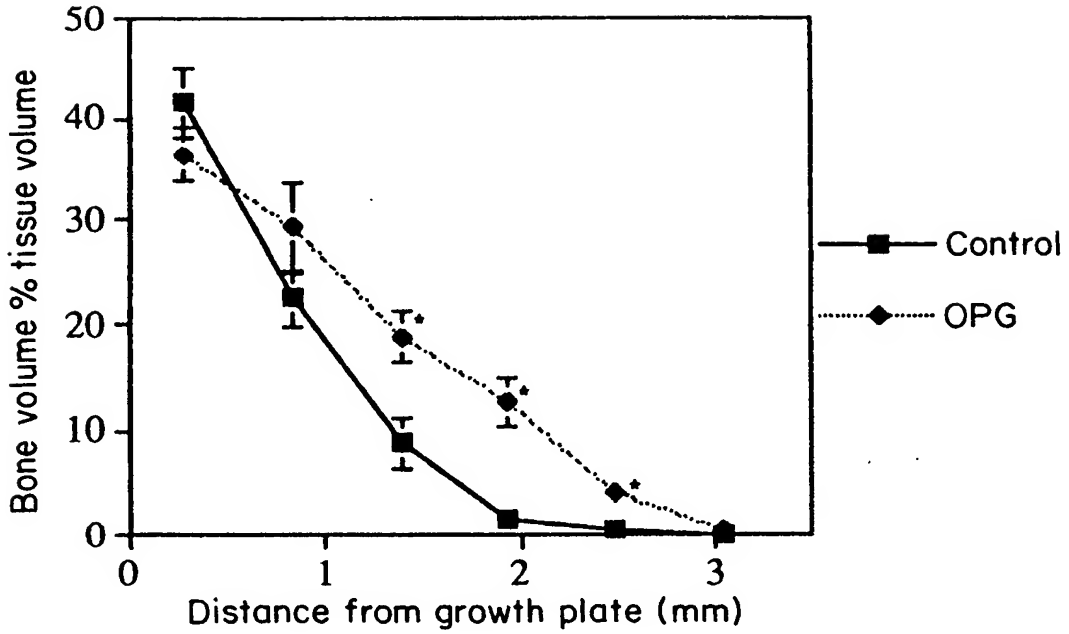


FIG.24B

FIG. 25



* Different to control $p < 0.01$

FIG.26A

FIG.26.B

FIG.27

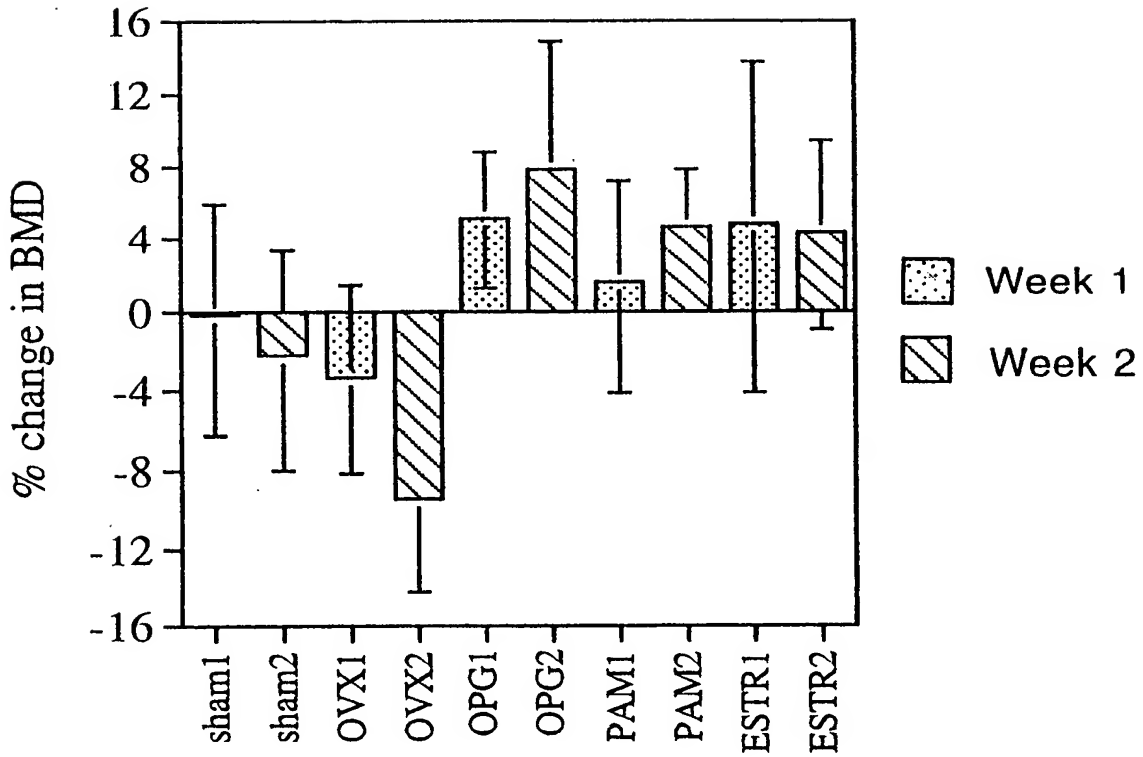
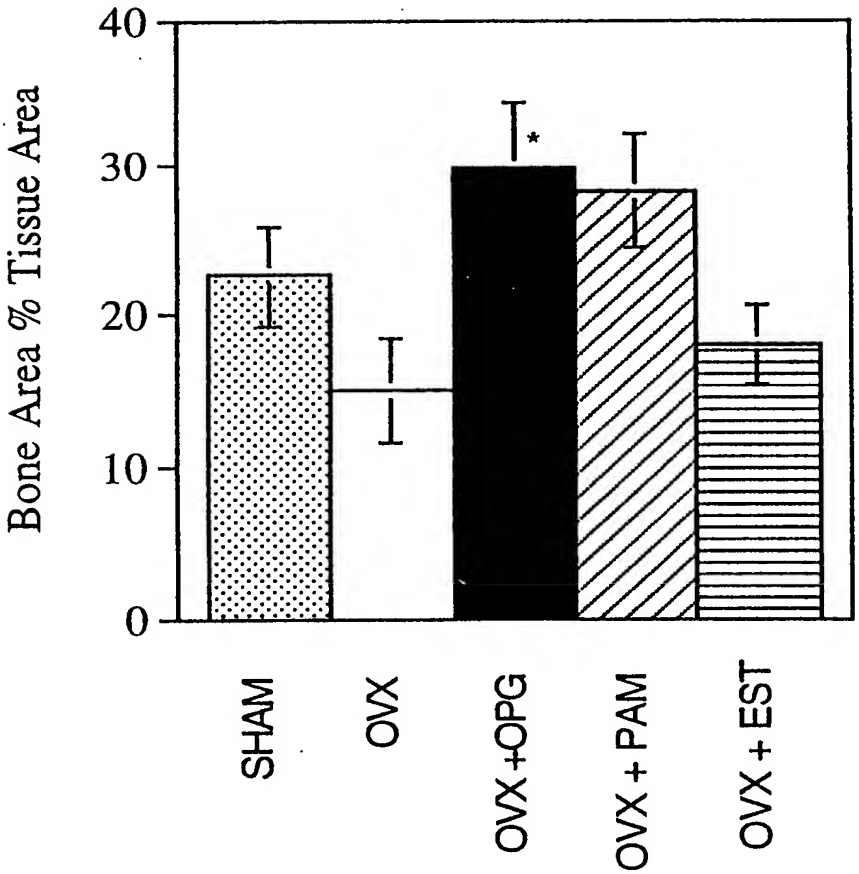

16
12
8
4
0
-4
-8
-12
-16
% change in BMD
sham1
sham2
OVX1
OVX2
OPG1
OPG2
PAM1
PAM2
ESTR1
ESTR2
Week 1
Week 2

FIG.28



* Different to OVX $p < 0.05$